

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:02:40 ; Search time 15.58 Seconds

(Without alignments)
740.893 Million cell updates/sec

Title: US-09-441-654a-1

Perfect score: 948

Sequence: 1 ADPRRSIHDFCLVSKVYGRG.....ACMLRCFRQENPPLIGSK 170

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_66:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	69.4	252	2 JG0185	hepatocyte growth
2	250.5	26.4	1558	2 T34384	hypothetical prote
3	250.5	26.4	2167	2 T34395	hypothetical prote
4	249.5	26.3	352	1 T1BOBI	alpha-1-microglobu
5	246.5	26.0	302	1 T1RTGK	tissue factor path
6	244.5	25.8	123	2 A29652	inter-alpha-trypsi
7	244.5	25.8	352	1 HCHU	alpha-1-microglobu
8	244	25.7	299	2 T46937	tissue factor path
9	243	25.6	300	2 SI2143	lipoprotein-associ
10	242.5	25.6	337	1 T1PGBI	alpha-1-microglobu
11	241.5	25.5	125	1 T1BOBI	alpha-1-microglobu
12	240	25.3	2225	2 T26063	hypothetical prote
13	239.5	25.3	396	2 S53325	tissue factor path
14	237.5	25.1	349	2 T21089	alpha-1-microglobu
15	236.5	24.9	304	1 T22264	tissue factor path
16	235.5	24.8	349	2 S35708	alpha-1-microglobu
17	233.5	24.6	304	1 T1H0GK	tissue factor path
18	222	23.4	1043	1 T19734	hypothetical prote
19	219	23.1	922	2 T23573	hypothetical prote
20	214.5	22.6	235	2 A54951	tissue factor path
21	210	22.2	765	2 T26880	amyloid precursor
22	209	22.0	1743	2 T26859	hypothetical prote
23	208	21.9	751	2 A49674	beta-amyloid precu
24	200	21.1	763	2 A49321	amyloid beta (A4)
25	200	21.1	1599	2 T16210	hypothetical prote
26	195	20.6	1391	2 T20406	hypothetical prote
27	193.5	20.4	111	2 S41082	amyloid precursor
28	193	20.4	284	2 S28291	hypothetical prote
29	186.5	19.7	747	2 JH0773	Alzheimer's disease

30	186	19.6	484	4 A32761	hypothetical prote
31	186	19.6	770	1 ORH0A4	Alzheimer's disease
32	185.5	19.6	1203	2 T21275	hypothetical prote
33	181.5	19.1	355	1 S22181	gamma-1-microglobu
34	178	18.8	1965	2 T33216	hypothetical prote
35	175.5	18.5	76	2 S03607	Alzheimer's disease
36	174.5	18.4	76	2 S04855	Alzheimer's disease
37	174.5	18.4	76	2 S06678	Alzheimer's disease
38	174.5	18.4	100	2 A32682	Alzheimer's disease
39	174.5	18.4	692	2 T32980	Alzheimer's disease
40	167	17.6	62	2 S07451	hypothetical prote
41	164	17.3	838	2 T20125	hypothetical prote
42	163.5	17.2	372	2 JC2556	alpha-1-microglobu
43	161	17.0	1208	2 T27822	hypothetical prote
44	159	16.8	265	2 A53350	Kunitz-type protei
45	156	16.5	64	2 S41399	Kunitz-type protei

ALIGNMENTS

RESULT 1

JG0185 hepatocyte growth factor activator inhibitor type 2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C/Accession: JG0185

R/Itch, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Koono, M.

Biochem. Biophys. Res. Commun. 255, 740-748, 1999

A/Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz

A/Reference number: JG0185; PMID:99160423

A/Accession: JG0185

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-252 <ITIO>

A/Cross-references: GB:AF099016

C/Superfamily: animal Kunitz-type proteinase inhibitor homology

F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 69.4%; Score 658; DB 2; Length 252;

Best Local Similarity 68.2%; Pred. No. 7.6e-52;

Matches 116; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY	1	ADPRRSIHDFCLVSKVYGRGCRASMPRMWYVDTGSCQLFYGGCDGNSNNYLKEECLK 60
DB	28	ASRELDVHESGVSQVSKYVGRKASIPRMWYVDTGSCQPFYGGCEGNGNYSKEECLK 87
QY	61	CATVENATGDLATSRNADSVSPAPRRDSEHSDMFNFEYCTANAVTGPCRASFP 120
DB	88	CAGVETNTYDDNARNRNGADSVLSPRKQSAEDLSAEIFNFEYCVKRAVTGPCRAFP 147
QY	121	RMYEDERNSCNNEITGGCRGNKNSRSEACMLRFRQENPPLIGSK 170
DB	148	RMYITDKNSCSFTYGGCRGNKNSYLSEACMQHSGRQMHPFLTPGLK 197

RESULT 2

T34394 hypothetical protein C37C3.6a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C/Accession: T34394

R/Giesel, C.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A/Description: The sequence of C. elegans cosmid C37C3.

A/Reference number: Z21518

A/Accession: T34394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1558 <GHI>

A/Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6

A/Experimental source: strain Bristol N2; clone C37C3

C:Genetics:
A:Gene: CESP:C37C3.6a
A:Map position: 5
A:Insertions: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1

Query Match
Best Local Similarity 30.1%; Score 250.5; DB 2; Length 1558;
Matches 49; Conservative 26; Mismatches 79; Indels 9; Gaps 1;

OY 5 RSIHDFCLVSKVVGRCASMPRMWNYNTDGSQLEFVYGCGDGNNNYLTKKECIKKC--- 61
Db 1265 QSMEDICRSRDAGPCPTYSDDWFYNAFSQELETFTTGGCGGNLNRFRSKDECEGRCFV 1324
62 -----ATTENATGDLATSRNADSSVPASPRRODSBDHSDMFNEYEECTANAVTGPG 115
OY 1325 HGAPSAARQEQAPAPAPAPAPAPPSNVSPPOQSASPVVYPNSKORDACHLNVDQGR 1384
Db 1385 KGAFDSWYEAVATGSCVTFFKYTCGGGANRFAKDCESLCVK 1427

OY 116 RASFPMWTFDVERNSCNNFTTYGCCRGKNKSYSEACMLRCR 158
Db 1385 KGAFDSWYEAVATGSCVTFFKYTCGGGANRFAKDCESLCVK 1427

RESULT 3
T34395
hypothetical protein C37C3.6b - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34395
R:Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C37C3.
A:Reference number: Z21518
A:Accession: T34395
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-2167 <GET>
A:Cross-references: EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C37C3.6b
A:Experimental source: Strain Bristol N2; clone C37C3
C:Genetics:
A:Gene: CESP:C37C3.6b
A:Map position: 5
A:Insertions: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/2

Query Match
Best Local Similarity 30.1%; Score 250.5; DB 2; Length 2167;
Matches 49; Conservative 26; Mismatches 79; Indels 9; Gaps 1;

OY 5 RSIHDFCLVSKVVGRCASMPRMWNYNTDGSQLEFVYGCGDGNNNYLTKKECIKKC--- 61
Db 1265 QSMEDICRSRDAGPCPTYSDDWFYNAFSQELETFTTGGCGGNLNRFRSKDECEGRCFV 1324
62 -----ATTENATGDLATSRNADSSVPASPRRODSBDHSDMFNEYEECTANAVTGPG 115
OY 1325 HGAPSAARQEQAPAPAPAPAPPSNVSPPOQSASPVVYPNSKORDACHLNVDQGR 1384
Db 1385 KGAFDSWYEAVATGSCVTFFKYTCGGGANRFAKDCESLCVK 1427

RESULT 4
TIPOBI
alpha-1-microglobulin / Inter-alpha-trypsin inhibitor precursor [validated] - bovine
N:Alternate names: BI-14 (inhibitory fragment of IRI), bikunin, ITI
C:Species: Bos primigenius taurus (cattle)
C:Date: 25-Feb-1985 #sequence_revision 04-Feb-2000 #text_change 18-Aug-2000
C:Accession: S68149; A91717; A90685; S31219; A01209
R:Lindqvist, A.; Akertstrom, B.
Biochim. Biophys. Acta 1306, 98-106, 1996
A>Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver
A:Reference number: S68149; MOID:96201710

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A:Accession: S68149
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-352 <LIN>
A:Cross-references: EMBL:U05642; NID:g1016297; PION:AAB07599.1; PID:g1016298
R:Hochstrasser, K.; Wachter, E.
H.Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A>Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
A:Reference number: A91717; MUID:84133807
A:Accession: A91717
A:Molecule type: Protein
A:Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC
R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A>Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
A:Reference number: A90685; MUID:85225967
A:Accession: A90685
A:Molecule type: Protein
A:Residues: 347-349 <HOC2>
R:Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A>Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
A:Reference number: A91718; MUID:84133808
A:Contents: annotation; reactive sites
R.Castillo, G.M.; Templeton, D.M.
FEBS Lett. 318, 292-296, 1993
A>Title: Subunit structure of bovine ESF (extracellular-matrix stabilizing factor)
A:Reference number: S31219; MUID:93178646
A:Accession: S31219
A>Status: preliminary
A:Molecule type: Protein
A:Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>
C:Superfamily: protein HC; animal kunitz-type proteinase inhibitor homology; lipocalin
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:35-188/Domain: lipocalin homology <lip>
F:231-281/Domain: animal kunitz-type proteinase inhibitor homology <BP1>
F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BP2>
F:241/inhibitory site: leu (chymotrypsin, elastase) #status experimental
F:250/binding site: carbohydrate (asn) (covalent) #status experimental
F:297/inhibitory site: Arg (trypsin) #status experimental

Query Match          26.3%; Score 249.5; DB 1; Length 352;
Best Local Similarity 32.4%; Pred. No. 4.2e-15;
Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps

OY      9  DFCLVSVKVGRCRASMPRMWYNVTGSCQLFYIYGCGDGSNNYLRKEELKKCATVENA 59
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      229 DSQLDPSOGPGICGLFKRFYFNGTSMACEFLFYGGGMGNFLSKBELQTCRTV---- 264

OY      69 TGDLATRNNAADSVSPAPRODSESHSDMFVEEYCETANAVTGFCRASFPFRMYEDVER 126
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      285 -----EACNLPITYGGRCRYIDLMAFDAAVK 309

OY      129 NSCNNFIYGCGRGNKNSYSNEACMLRC 156
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      310 GKCVRFSGGCKGNGNKFYSEKECKEYC 337

RESULT 5
TIRTKG
tissue factor pathway inhibitor precursor - rat
N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
C:Accession: JX0213
R:Enyoji, K.; Emi, M.; Mukai, T.; Kato, H.
J. Biochem. 111, 681-687, 1992
A>Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).
A:Reference number: JX0213; MUID:92348361
A:Accession: JX0213
A:Molecule type: mRNA.
A:Residues: 1-302 <END>
```

A:Cross-references: DDBJ:D10926; NID:g220916; PIDN:BA01724.1; PID:g220917
 A:Experimental source: liver
 C:Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent in

C:Superfamily: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
 C:Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>
 F:53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:288-291/Region: heparin binding #status predicted
 F:33-103/62-86/78-99/124-174/133-157/149-170/222-272/231-255/247-268/disulfide bonds: #S
 F:134/inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predict
 F:144/251/261/Binding site: carbonylate (Asn) (covalent) #status predicted
 F:222/inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 26.0% Score 246.5; DB 1; Length 302;
 Best Local Similarity 34.0% Pred. No. 6.7e-15;
 Matches 54; Conservative 21; Mismatches 65; Indels 19; Gaps 3;

OY 9 DPLVSVVRCRASPFRMYNTDGSQOLFVYGGCDGNSNNYTKRECKKCA-TTEN 67
 DB 122 DFCFLDEDPICRGFMTRFYFNQSKQCFQKYGGLGNSNNFTLECNTECDPVNEY 181
 OY 68 ATGDLATSR-----NAADSVSPARRDSEHSDMFNYEECTANAVTGPCRA 117
 DB 182 QKGDYTNQITVDTTNNVTPQATKASQWDYDGP-----WCLEPDSGLCKA 233
 OY 118 SEPRTFEDVRNSCNFFYGGCGNKNRSYSEACMLRC 156
 DB 234 SEKRFYNPAIGKCRGFNYTGCGGNNNNFTTKDCNRC 272

RESULT 6
 A29652
 Inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
 C:Accession: A29652
 R:RSP, G.; Hochstrasser, K.; Wachter, E.; Reisinger, P.W.M.
 Biol. Chem. Hoppe-Seyler 368, 727-731, 1987
 A:Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha-
 sin inhibitor, XI.
 A:Reference number: A29652; MUID:87299012
 A:Accession: A29652
 A:Molecule type: protein
 A:Residues: 1-123 <RAS>
 C:Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin h
 C:Keywords: serine proteinase inhibitor
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match 25.8% Score 244.5; DB 2; Length 123;
 Best Local Similarity 31.8% Pred. No. 4e-15;
 Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;

OY 9 DPLVSVVRCRASPFRMYNTDGSQOLFVYGGCDGNSNNYTKRECKKCA-TYENA 68
 DB 3 DSCQLYSGPCLGMFRFYNGTSMACETFFYGGCGNKNNSPEKCLQTRTV--- 58
 OY 69 TGLDATSRNADSSVSPARRDSEHSDMFNYEECTANAVTGPCRA-SFPRTYDVER 128
 DB 59 -----OACNLPYRGPCRAIGIELMADAVK 83
 OY 129 NSCNNTYGGCGNKNRSYSEACMLRC 156
 DB 84 GRCVRFYGGCGNKNRSYSEACMLRC 111

RESULT 7
 HCHU

alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - human
 N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC
 rich protein
 C:Contents: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
 C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text_change 04-Feb-2000
 C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; PNO450; B39079; A61520;
 3217

R:Ver, H.; Gebhard, W.
 Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
 A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
 A:Reference number: S13433; MUID:91214554
 A:Accession: S13433

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-352 <VERTJ>

A:Cross-references: EMBL:X54816; NID:g24475; PIDN:CAA38585.1; PID:g825614; EMBL:X54816
 R:Diara-Mehpour, M.; Bouguignon, J.; Seebouee, R.; Salier, J.P.; Leveillard, T.; M
 Eur. J. Biochem. 191, 131-139, 1990
 A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain g
 A:Reference number: S10778; MUID:90336621
 A:Accession: S10778

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-202 <DIA>
 R:Kunne, J.F.; Polazzi, J.O.; Kotlick, M.P.
 Nucleic Acids Res. 14, 7839-7850, 1986

A:Title: The mRNA for a proteinase inhibitor related to the H1-30 domain of inter-
 A:Reference number: A93642; MUID:87040757
 A:Accession: A93642

A:Molecule type: mRNA
 A:Residues: 1-352 <KAU>
 A:Cross-references: SB:X04494; NID:g24478; PIDN:CAA28182.1; PID:g244479
 R:Lopez-Otin, C.; Grubb, A.O.; Mendez, E.
 Arch. Biochem. Biophys. 228, 544-554, 1984

A:Title: The complete amino acid sequence of human complex-forming glycoprotein
 A:Reference number: A90074; MUID:84126849
 A:Accession: A90074

A:Molecule type: protein
 A:Residues: 20-56,58-202 <LOP>
 A:Experimental source: individual with tubular proteinuria
 A>Note: no evidence of sequence heterogeneity could be found, in spite of presence
 R:Tagaki, T.; Takagi, K.; Kawai, T.
 Biochem. Biophys. Res. Commun. 98, 997-1001, 1981

A:Title: Complete amino acid sequence of human alpha-1-microglobulin.
 A:Reference number: A90225; MUID:81184038
 A:Accession: A90225

A:Molecule type: protein
 A:Residues: 20-47,58-136,138-141,143-144,146-198 <TAK>
 A:Experimental source: pooled urine of patients with tubular proteinuria
 R:Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempar, K.; Salier, C.
 Biol. Chem. Hoppe-Seyler 366, 479-483, 1985

A:Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type
 A:Reference number: A90686; MUID:85225968
 A:Accession: A90686

A:Molecule type: protein
 A:Residues: 206-290,VI,293-342,III,344-350 <REI>
 R:Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Druce, T.; Daudon, M.
 Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993

A:Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor
 A:Reference number: PNO450; MUID:93221481
 A:Accession: PNO450

A:Molecule type: protein
 A:Residues: 206-214,X' <ATM>
 R:Englind, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S
 J. Biol. Chem. 266, 747-751, 1991

A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood p
 A:Reference number: A39079; MUID:91093267
 A:Accession: B39079
 A:Molecule type: protein
 A:Residues: 206-225 <ENG1>

R.Chirat, F.; Baldyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
Int. J. Biochem. 23, 1201-1203, 1991
A:Title: A chondroitin sulfate chain is located on serine-10 of the urinary trypsin inhibitor
A:Reference number: A61580; MUID:92175157
A:Accession: A61580
A:Molecule type: protein
A:Residues: 214, 'X', 216-222, 'X' <CH1>
R.McKeenan, W.L.; Sakagami, Y.; Hoshi, H.; McKeenan, K.A.
J. Biol. Chem. 261, 5378-5383, 1986
A:Title: Two apparent human endothelial cell growth factors from human hepatoma cells at
A:Reference number: A92583; MUID:8618278
A:Accession: B25604
A:Molecule type: protein
A:Residues: 206-214, 'X', 216-230, 'X', 232-239, 'X', 241-248, 'XX', 251-252, 'X', 254 <MCK>
R.Engelild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
A:Reference number: A92736; MUID:89380192
A:Accession: C34245
A:Molecule type: protein
Residues: 206-225 <ENG2>
Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A:Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobulin)
A:Reference number: A25303; MUID:86312901
A:Accession: A25303
A:Molecule type: mRNA
A:Residues: 1-218, 'HW' <TRA>
A:Note: this mRNA sequence appears to contain errors after residue 218
R.Calero, M.; Escribano, J.; Grubb, A.; Mendez, E.
J. Biol. Chem. 269, 384-389, 1994
A:Title: Location of a novel type of interpolypeptide chain linkage in the human protein
A:Reference number: A53110; MUID:94103241
A:Accession: A53110
A:Molecule type: protein
A:Residues: 45-57 <CAL>
R.Veier, H.; Koegler, M.; Gebhard, W.
FEBS Lett. 245, 137-140, 1989
A:Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhib
A:Reference number: S03552; MUID:89171290
A:Accession: S03552
A:Status: nucleic acid sequence not shown
A:Status: preliminary
A:Molecule type: protein
A:Residues: 206-352 <VET2>
R.Malki, N.; Baldyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fournie
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A:Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation
A:Reference number: S28928; MUID:93039735
A:Accession: S28928
A:Status: preliminary
A:Molecule type: protein
A:Residues: 206-215 <AAL>
R.Morille, W.; Capon, C.; Baldyck, M.; Sautiere, P.; Kowach, M.; Michalski, C.; Fournie
Eur. J. Biochem. 221, 881-888, 1994
A:Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of int
A:Reference number: S43466; MUID:94229087
A:Accession: S43466
A:Status: preliminary
A:Molecule type: protein
A:Residues: 206-221 <MOR>
R.Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vliet, J.
Biochemistry 33, 7423-7429, 1994
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp
A:Reference number: A53642; MUID:94271799
A:Accession: A53642
A:Status: preliminary
A:Molecule type: protein
A:Residues: 206-217 <WIS>
R.Calero, M.; Mendez, E.; Garcia, E.
Biochim. Biophys. Acta 1249, 91-99, 1995
A:Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
A:Reference number: S55688; MUID:95284116
A:Accession: S55688

A:Molecule type: protein
A:Residues: 20-24 <CAL2>
R.Bourguignon, J.; Daria-Mehrpour, M.; Seabone, R.; Frain, M.; Sala-Trepat, J.M.; Ma
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1995
A:Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide
A:Reference number: 152208; MUID:86025577
A:Accession: 152208
A:Status: translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 302-352 <BOU>
A:Cross-references: GB:M11562; NID:g186587; PIDN:AA59194.1; PID:9307077
R.Mojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Pe
Biochem. J. 311, 753-759, 1995
A:Title: Factor IX Zúñigen: a Cys(18) -> Arg mutation results in formation of a heter
A:Reference number: S59509; MUID:96067589
A:Accession: S59509
A:Molecule type: protein
A:Residues: 27-35, 'Y', 37 <MOJ>
R.Aramant, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A:Title: Identification of uronic-acid-rich protein as urinary bikunin, the light cha
A:Reference number: S66434; MUID:96270753
A:Accession: S66434
A:Molecule type: protein
A:Residues: 206-214, 'X', 216-230 <ATM2>
R.Akersstroem, B.; Bratt, T.; Engelild, J.J.
FEBS Lett. 362, 50-54, 1995
A:Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect
A:Reference number: S68728; MUID:95212582
A:Accession: S68728
A:Molecule type: protein
A:Residues: 89-100 <AKE>
R.Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor
A:Reference number: S02431; MUID:88167187
A:Accession: S02431
A:Molecule type: protein
A:Residues: 206-214, 'X', 216-217 <JES>
R.Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A:Title: Human protein HC displays variability in its carboxyl-terminal amino acid se
A:Reference number: A91304
A:Contents: annotation: variant of alpha-1-microglobulin
A:Note: pooled urine samples contained two forms of this protein, both lacking 57-Tyr
R.Hochstrasser, K.; Schonberger, O.L.; Rossmann, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the
A:Reference number: A91698; MUID:82074265
A:Contents: annotation: carbohydrate binding sites
R.Morille, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A:Title: The reactive site of human inter-alpha-trypsin inhibitor is in the
A:Reference number: A90687; MUID:85225940
A:Contents: annotation: inhibitory site
A:Note: in vitro, the first twelve residues of the amino end of the inhibitor
A:Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytic
C:Comment: Alpha-1-microglobulin occurs in many physiological fluids including
It contains at least one brown-yellow chromophore.

Query Match 25.8%; Score 244.5; DB 1; Length 352;
Best Local Similarity 32.8%; Pred No.12e-14;
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;
DB 229 DSCQLGYAGCMGMRTRYNGNSMACETFGCGCMGNFVEKEBLCQCRFVAA-- 286
9 DFCVSKVYGRASPRMWNVTYDSCQLFYVGGCGNSNNYLKREDCIKKCATVENA 68
DB 229 DSCQLGYAGCMGMRTRYNGNSMACETFGCGCMGNFVEKEBLCQCRFVAA-- 286
QY 69 TGDLATSNAPADSSVPAPRROSESDHSSMFEYEEYCANNAVTCGRASPRFWYDVER 128
DB 287 -----CNLFYVGRCAFLQTMADFAYK 309

QY 129 NSCNFIYGGCGRNKSYRSEACMLRC 156
 Db 310 GKCVLFPGCGCGNGNKFYSSECKEYEC 337

RESULT 8

I46937
 Tissue factor pathway inhibitor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
 C:Accession: I46937
 R:Belasouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
 Thromb. Res. 69, 547-553, 1993
 A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
 A:Reference number: I46937; MUID:93276427
 A:Accession: I46937
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-299 <BEL>
 Cross-references: GB:S61902; NID:q386015; PIDN:AAB26836.1; PID:q386016
 Superfamily: Tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 F:49-59/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>

Query Match 25.7%; Score 244; DB 2; Length 299;
 Best Local Similarity 30.0%; Pred. No. 1.1e-14;
 Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

QY 4 ERSIHDFCLVSKVGRASMPRMWYNVTDGSCOLFVYGGCGDGSNNYLTKECLKCAT 63
 Db 42 QKPTHSFCAMKVDGDCRCRYIKRFNNILAHQCEEFYGGCGENNFESLECKEKCAC 101
 QY 64 VTEANATGLATSRNAADSVSPAPRRDSEDSMDENYECYANAVTGPCRASPPRMV 123
 Db 102 DYPMATTKLTFQKGRPD-----FCFLDEDPGICRCYITRYF 137
 QY 124 FDEVRNSCNFIYGGCGRNKSYRSEACMLRCFROENP 163
 Db 138 YNNSKQCEKRFKYGCGCLGNLNFESLECKKNTC---ENP 173

RESULT 9

I512143
 lipoprotein-associated coagulation inhibitor precursor - rabbit
 A:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C:Accession: S12143; A61373
 R:Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
 Nucleic Acids Res. 18, 6440, 1990
 A:Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
 A:Reference number: S12143; MUID:91057146
 A:Accession: S12143
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-300 <WES>
 A:Cross-references: EMBL:X54708; NID:q1612; PIDN:CAA8515.1; PID:q1613
 R:Colburn, P.; Grab, J.W.; Buonassisi, V.
 J. Cell. Physiol. 148, 320-326, 1991
 A:Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell
 A:Reference number: A61373; MUID:91349227
 A:Accession: A61373
 A:Molecule type: protein
 A:Residues: 25-33, 'X', '35-46 <COL>
 C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 F:50-100/Domain: anticoagulant; glycoprotein
 F:121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 25.6%; Score 243; DB 2; Length 300;
 Best Local Similarity 30.0%; Pred. No. 1.4e-14;
 Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

QY 4 ERSIHDFCLVSKVGRASMPRMWYNVTDGSCOLFVYGGCGDGSNNYLTKECLKCAT 63
 Db 43 QKPTHSFCAMKVDGDCRCRYIKRFNNILAHQCEEFYGGCGENNFESLECKEKCAC 102
 QY 64 VTEANATGLATSRNAADSVSPAPRRDSEDSMDENYECYANAVTGPCRASPPRMV 123
 Db 103 DYPMATTKLTFQKGRPD-----FCFLDEDPGICRCYITRYF 138
 QY 124 FDEVRNSCNFIYGGCGRNKSYRSEACMLRCFROENP 163
 Db 139 YNNSKQCEKRFKYGCGCLGNLNFESLECKKNTC---ENP 174

RESULT 10

I1P6B1
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
 A:Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: S11066; S13493; A01208
 R:Gebhard, W.; Schreimüller, T.; Vetr, H.; Wächter, E.; Hochstrasser, K.
 FEBS Lett. 269, 32-36, 1990
 A:Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microgl
 A:Reference number: S11066; MUID:90353595
 A:Accession: S11066
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-337 <GEB>
 A:Cross-references: EMBL:X53685; NID:q1877; PIDN:CAA37725.1; PID:q1878
 R:Tavakoli, A.
 Biochim. Biophys. Acta 1088, 47-56, 1991
 A:Title: Molecular cloning of porcine alpha(1)-microglobulin/Hi-30 reveals developmen
 A:Reference number: S13493; MUID:91113729
 A:Accession: S13493
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'M', '3-48', 'M', '50-337 <TAV>
 A:Cross-references: GB:X52087; NID:q1881; PIDN:CAA6306.1; PID:q1882
 A:Note: The authors translated the codon GTG for residue 2 as a Met initiation codon.
 R:Hochstrasser, K.; Wächter, E.; Albrecht, G.J.; Reisinger, P.
 Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
 A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
 A:Reference number: A90685; MUID:85225967
 A:Accession: A01208
 A:Molecule type: protein
 A:Residues: 212-258, 'Q', '260-269', 'S', '271-277', 'Q', '279-282', 'A', '284', 'IR', '287-292', 'A', '294-
 C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
 C:Comment: The amino acid at position P2 (228-Met) appears to determine the specific
 C:Comment: elastase; those with leucine interact strongly.
 C:Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology: I:pep
 C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
 F:20-173/Domain: lipocalin homology <LIP>
 F:216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:316-266, 225-249, 241-262, 272-322, 281-305, 297-318/Disulfide bonds: #strains pre:
 F:236/Inhibitory site: Leu (chymotrypsin, elastase) #status pre:
 F:235/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 25.6%; Score 242.5; DB 1; Length 337;
 Best Local Similarity 31.8%; Pred. No. 1.7e-14;
 Matches 47; Conservative 19; Mismatches 43; Indels 39; Gaps

QY 9 DECLVSKVGRASMPRMWYNVTDGSCOLFVYGGCGDGSNNYLTKECLKCATYTENA 68
 Db 214 DSCGLGYSQSGPCLGMKRFYNGSSMACETFRHGGCGNGNFSKELQTCRTV---- 269

QY 69 TGLDLSRNADSSVPSAPRRODSEHSDMFNEEYECTANAVTGPCRASFPMWYDVER 128
 Db 270 -----EACSLPIYSGPCRGFFQJMAFDVAQ 294
 QY 129 NSCNFFIYGGCRGNKNSYSEACMLRC 156
 Db 295 GKCVLFYGGCGNGNGNFYSKECKEYIC 322
 RESULT 11
 TIRHOBI
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
 N:Alternate names: EI-14 (inhibitory fragment of IRI); IRI; trypsin inhibitor, E-UTI
 C:Species: Equus caballus (domestic horse)
 C>Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 05-May-2000
 C:Accession: A01210; A45653
 R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
 Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
 Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
 A:Reference number: A90685; MUID:85225967
 A:Accession: A01210
 A:Molecule type: protein
 A:Residues: 3-125 <HOC>
 R:Veeraratnam, K.; Singh, K.; Wachter, E.; Hochstrasser, K.
 Biochem. Int. 26, 405-413, 1992
 A:Title: Characterization of a trypsin inhibitor from equine urine.
 A:Reference number: A45653; MUID:92328613
 A:Accession: A45653
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12, E', 14-33 <VEE>
 A:Cross-references: PIDN:AB22430.1; PID:g250858
 A:Experimental source: urine
 A:Note: sequence extracted from NCBI backbone (NCBI:107966)
 C:Comment: This inhibitory fragment, released from native IRI after limited proteolysis
 first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
 C:Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
 d elastase: those with leucine interact strongly.
 C:Superfamily: protein HC; animal kunitz-type proteinase inhibitor homology; lipocalin h
 C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
 F:7-57/Domain: animal kunitz-type proteinase inhibitor homology <BP1>
 F:63-113/Domain: animal kunitz-type proteinase inhibitor homology <BP2>
 F:57-16-40,32-53,63-113,72-96,88-109/Distulfide bonds: #status predicted
 F:17/inhibitory site: Leu (chymotrypsin, elastase) #status predicted
 F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:73/inhibitory site: Arg (trypsin) #status predicted

submitted to the EMBL Data Library, March 1997
 A:Reference number: 220145
 A:Accession: T26063
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2225 <WIL>
 A:Cross-references: EMBL:292815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
 A:Experimental source: clone W01F3
 C:Genetics:
 A:Gene: CESP:W01F3.3
 A:Map position: 5
 A:Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1176/1; ---

Query Match 25.3%; Score 240; DB 2; Length 2225;
 Best Local Similarity 29.3%; Pred. No. 2, 1e-13;
 Matches 46; Conservative 21; Mismatches 58; Indels 32; Gaps 2;
 QY 11 CLVSKVYGRCHASMPRMWYNTDSCQLFYVGGCGDGSNNYLTKEECLKKC--ATVENA 69
 Db 777 CLHPRDSGNCNGQVRFNFDEKKNCDVFTYGCQGNNGNFASKEDCMATCKRKEPTPSA 834
 QY 69 TGLDLSRNADSSVPSAPRRODSEHSDMFNEEYECTANAVTGPCRASFPMWYDVER 128
 Db 837 TPD-----FSQCSNDVDAGECNGVFERAFDALA 663
 QY 129 NSCNFFIYGGCRGNKNSYSEACMLRCFROENPPL 165
 Db 867 ODCRAFTYGGCGNGNNTATMQECSRVMAMKSPV 903

RESULT 13
 S53325
 Tissue factor pathway inhibitor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
 C:Accession: S53325
 R:Girard, J. J.; Gailani, D.; Broze Jr., G. J.
 Biochem. J. 303, 923-928, 1994
 A:Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor revea
 A:Reference number: S53325; MUID:95071310
 A:Accession: S53325
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-336 <GIR>
 C:Superfamily: animal kunitz-type proteinase inhibitor homology
 C:Keywords: serine proteinase inhibitor
 F:53-103/Domain: animal kunitz-type proteinase inhibitor homology <BP2>
 F:125-175/Domain: animal kunitz-type proteinase inhibitor homology <BP3>
 F:309-359/Domain: animal kunitz-type proteinase inhibitor homology

Query Match 25.3%; Score 239.5; DB 2; Length 396;
 Best Local Similarity 29.6%; Pred. No. 3, 8e-14;
 Matches 45; Conservative 24; Mismatches 60; Indels 23; Gaps 1;
 QY 5 RSHDPLVSKVYGRCHASMPRMWYNTDSCQLFYVGGCGDGSNNYLTKEECLKKATV 64
 Db 47 RLHSFALKADNGPCRAMIRNFNFHITQCEEFYGGCEGNGNRFESIECEKCVRV 106
 QY 65 TENATGLDLSRNADSSVPSAPRRODSEHSDMFNEEYECTANAVTGPCRASFPMWY 124
 Db 107 YPKA-----KTELEKLEKPDCHNNEDSGLCRGVTRYKY 143
 QY 125 DYERNSCNFFIYGGCRGNKNSYSEACMLRC 156
 Db 144 NNVSSKCEGFKYGGGLGNLNFETIEQCKNTC 175

RESULT 14
 S51089
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor - rat
 N:Alternate names: acid-stable proteinase inhibitor; bikunin; tryptstatin
 R:Cummings, P.

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
 C:Accession: S21089; A53056; A25935; A31890; A61633
 R:Linkqvist, A.; Bratt, T.; Allert, M.; Kaster, W.; Akerstrom, B.
 R:Biochem. Biophys. Acta 1130, 63-67, 1992
 A:Title: Rat alpha(1)-microglobulin co-expression in liver with the light chain of inter-alpha(1)-microglobulin
 A:Reference number: S21089; MUID:92182014
 A:Accession: S21089
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-349 <LIN>
 A:Cross-references: GB:S87544; NID:q247162; PID:AMB21782.1; PID:q247163
 J:Biochem. Biophys. Acta 1130, 63-67, 1992
 J:Biochem. Biophys. Acta 1130, 63-67, 1992
 J:Biochem. Biophys. Acta 1130, 63-67, 1992
 A:Title: Mast cell protease inhibitor, trypsin, is a fragment of inter-alpha-trypsin
 A:Reference number: A53056; MUID:9414892
 A:Accession: A53056
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 285-341 <ITD>
 R:Kaster, W.; Bjorck, L.; Akerstrom, B.
 J:Biochem. Biophys. Acta 1130, 63-67, 1992
 A:Title: Developmental and tissue-specific expression of alpha-1-microglobulin mRNA in rat
 A:Reference number: A25935; MUID:87033744
 A:Accession: A25935
 A:Molecule type: protein
 A:Residues: 141, 'A', '143-195 <KAS>
 R:Kido, H.; Yokogoshi, Y.; Katunuma, N.
 J:Biochem. Biophys. Acta 1130, 63-67, 1992
 A:Title: Kunitz-type protease inhibitor found in rat mast cells. Purification, properties
 A:Reference number: A31890; MUID:89053978
 A:Accession: A31890
 A:Molecule type: protein
 A:Residues: 283-301, 'L', '303-322, 'N', '324-329, 'PK', '332-333, 'W', '335-343 <KID>
 R:Sugiki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Mahara, H.
 J:Biochem. Biophys. Acta 1130, 63-67, 1992
 A:Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflammation
 A:Reference number: A61633; MUID:92120777
 A:Accession: A61633
 A:Molecule type: protein
 A:Residues: 205-213, 'X', '215-229, 'N', '231-232, 'K', '234-238 <SUG>
 C:Superfamily: protein HC, animal Kunitz-type proteinase inhibitor homology; lipocalin
 C:Keywords: chondroitin sulfate proteoglycan; chromoprotein; glycoprotein; plasma; serin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-202/Product: alpha-1-microglobulin #status predicted <AIM>
 F:34-187/Domain: lipocalin homology <LIP>
 F:203-349/Product: inter-alpha-trypsin inhibitor #status experimental <IAI>
 F:230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:52/Cross-link: alpha-1-microglobulin-ig alpha complex chromophore (Cys) (interchain to
 F:114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:124/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
 F:296/Inhibitory site: Arg (trypsin) #status predicted

Query Match 25.1%; Score 237.5; DB 2; Length 349;
 Best Local Similarity 30.4%; Pred. No. 5e-14;
 Matches 45; Conservative 17; Mismatches 47; Indels 39; Gaps 1;
 QY 9 DFCVSKVYGRCSRASMPRMWNTDSCQLFYGGGDSNNYLTKECLKCAVTEA 68
 Db 228 DSCQLNYSSEGLCMQKYYTNGASMCETFOYGGCLGNGNMFASKEKCLQTCRTIAA-- 285
 QY 69 TGLDLSRNADSSVPSAPRRDSEHSDMFNFEYCTANAVTPGCRASPRRYE 128
 Db 286 -----CNLPYOGPCRAFAELMAFDAAQ 308
 QY 129 NSCNFFIYGGCRGNKNSYRSEACMLRC 156
 Db 309 GKCIQFIYGGCRGNKNSYRSEACMLRC 336

RESULT 15
 JC2264
 tissue factor pathway inhibitor precursor - rhesus macaque
 N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation in
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 A:Accession: JC2264
 R:Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miy
 J:Biochem. Biophys. Acta 1130, 63-67, 1992
 A:Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor
 A:Reference number: JC2264; MUID:94375417
 A:Accession: JC2264
 A:Molecule type: mRNA
 A:Residues: 1-304 <KAM>
 A:Cross-references: GB:S73337; NID:9685016; PID:AMB31955.1; PID:9685017
 A:Experimental source: liver
 C:Comment: This protein inhibits the activities of factor Xa and tissue factor-
 C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase
 C:Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
 F:54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
 F:54-104,63-87,79-100,125-175,134-156,150-171,217-267,226-250,242-263/Disulfide bonds
 F:64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status pred
 F:135/Inhibitory site: Arg (coagulation factor X) #status predicted
 F:145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 24.9%; Score 236.5; DB 1; Length 304;
 Best Local Similarity 34.9%; Pred. No. 5.3e-14;
 Matches 53; Conservative 24; Mismatches 64; Indels 11; Gaps
 QY 9 DFCVSKVYGRCSRASMPRMWNTDSCQLFYGGGDSNNYLTKECLKCAVTEA 68
 Db 123 DFCLEEDGICRGYTRFYNNQSKCRFRYGGCLGNNMFETLECKNTC---EDG 172
 QY 69 TG-----DLATSRNADSSVPSAPRRDSEHSDMFNFEYCTANAVTPGCRASPRRYE 124
 Db 180 NQFYDNDGTQJNVAVNS--QTP--QSTKVPSEFFHGPSWCLAPADRGCLCANENRFLY 235
 QY 125 DVERNSCNFFIYGGCRGNKNSYRSEACMLRC 156
 Db 236 NSVICKCRPFKISGGCGNENFTSKRECLRAC 267

Search completed: January 31, 2001, 15:03:23
 Job time: 43 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:03:08 ; Search time 10.15 Seconds

(without alignments)
540.886 Million cell updates/sec

Title: US-09-441-654A-1

Perfect score: 948

Sequence: 1 ADERSIHDFCLVSKVGVRC.....ACMLRCFRQENPPLGSK 170

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Minimum number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	249.5	26.3	352	1	AMBP_BOVIN
2	247.5	26.1	346	1	AMBP_MERON
3	246.5	26.0	302	1	TFPI_RAT
4	244.5	25.8	123	1	IATR_SHEEP
5	244.5	25.8	352	1	AMBP_HUMAN
6	244.5	25.7	300	1	TFPI_RABTT
7	242.5	25.6	337	1	AMBP_PIG
8	241.5	25.5	123	1	IATR_HORSE
9	237.5	25.1	349	1	AMBP_RAT
10	236.5	24.9	304	1	TFPI_MACMU
11	235.5	24.8	349	1	AMBP_MESAU
12	235.5	24.8	349	1	AMBP_MOUSE
13	233.5	24.6	304	1	TFPI_HUMAN
14	214.5	22.2	765	1	TFPI_HUMAN
15	210	22.2	765	1	TFPI_RAT
16	200	21.1	763	1	TFPI_RAT
17	191	20.1	1416	1	YNB1_CAMEL
18	187.5	19.8	770	1	A4_RAT
19	186	19.6	751	1	A4_SAISC
20	183.5	19.4	770	1	A4_HUMAN
21	183.5	19.4	770	1	A4_MOUSE
22	181.5	19.1	355	1	AMBP_PIEPL
23	175.5	18.5	69	1	CRPT_BOOMT
24	174.5	18.4	76	1	A4_MACMU
25	174.5	18.4	76	1	A4_MACMU
26	167	17.6	87	1	IP52_MACFA
27	159	16.8	265	1	TKD1_SHEEP
28	156	16.5	64	1	TKD1_HUMAN
29	155	16.4	164	1	TKD1_BOVIN
30	155	16.4	60	1	IBPS_BOVIN
31	153	16.1	100	1	IBPI_TACTR
32	153	16.1	100	1	IBPI_BOVIN
33	152.5	16.1	100	1	IBPI_BOVIN

34	152	16.0	65	1	IVB3_VIPAA	P00992 vipera ammoo
35	150.5	15.9	60	1	IVB2_DABRU	P00990 dabola russ
36	150.5	15.9	122	1	UPT1_PIG	Q29100 sus scrofa
37	150	15.8	110	1	IBP_CARCR	P00993 carctis r
38	149	15.7	61	1	IVB1_VIPAA	P00994 vipera ammoo
39	147	15.5	58	1	ISIK_HELPO	P00976 helix scro
40	147	15.5	67	1	IBPC_BOVIN	P00976 bos taurus
41	145	15.3	55	1	ISH_STOHE	P8129 stochellic
42	145	15.3	62	1	IVB2_STOHE	P24341 eristocopa
43	143	15.1	83	1	IVB2_ERMA	P02845 macropus m
44	142	15.0	83	1	ELAC_MACMU	P15989 gallus gall
45	141	14.9	65	1	IVB1_BUNFA	P25660 bunnellus m

ALIGNMENTS

RESULT	1	STANDARD	PRT	352 AA.
ID	AMBP_BOVIN			
AC	P00978; P35420; Q28020;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	AMBP PROTEIN PRECURSOR (CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-TRYPsin INHIBITOR LIGHT CHAIN (ITI-1C) (BIKUNIN) (HI-30) (BI-14) (CUMULUS EXTRACELLULAR MATRIX STABILIZING FACTOR) (ESF)).			
GN	AMBP OR ITIL.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
CC	Bovidae; Bovinae; Bos.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=96201710; PubMed=8611630;			
RA	Lindqvist A., Akerstrom B.;			
RT	"Bovine alpha 1-microglobulin/bikunin. Isolation and characterization of liver cDNA and urinary alpha 1-microglobulin.";			
RL	Biochim. Biophys. Acta 1306:98-106(1996).			
RN	[2]			
RN	SEQUENCE OF 227-349.			
RP	MEDLINE=85225967; PubMed=2408637;			
RX	Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;			
RA	"Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the trypsin-released inhibitors from horse and pig inter-alpha-trypsin inhibitors.";			
RT	Biol. Chem. Hoppe-Seyler 366:473-478(1985).			
RL	[3]			
RN	SEQUENCE OF 227-348.			
RP	MEDLINE=84133807; PubMed=6199275;			
RX	Hochstrasser K., Wachter E.;			
RA	"Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, VII. Determination of the amino-acid sequence of the trypsin-released inhibitor from bovine inter-alpha-trypsin inhibitor.";			
RT	Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).			
RL	[4]			
RN	SEQUENCE OF 206-219.			
RP	TISSUE=FETAL SERUM;			
RX	MEDLINE=92281130; PubMed=1376324;			
RA	Chen L., Mo S.-J.T., Larsen W.O.;			
RT	"Identification of a factor in fetal bovine serum that stabilizes the cumulus extracellular matrix. A role for a member of the inter-alpha-trypsin inhibitor family.";			
RL	J. Biol. Chem. 267:12380-12386(1992).			
RN	[5]			
RP	REACTIVE SITES.			
RX	MEDLINE=84133803; PubMed=6199276;			
RA	Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;			
RT	"Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, VII. Characterization of the			

FT			bovine inhibitor as double-headed trypsin-elastase inhibitor.";
Rt			Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).
-1			FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA AND ALBUMIN.
-1			FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC ELASTASE.
-1			FUNCTION: MAY DIFFUSE INTO FOLLICULAR FLUID AFTER AN OVULATORY STIMULUS TO ACT AS STRUCTURAL LINKER THAT ENSURE NORMAL CUMULUS EXPANSION, THROUGH STABILIZATION OF THE CUMULUS EXTRACELLULAR MATRIX THUS SUPPORTING THE PROCESS OF OOVULATION.
-1			PMT: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO SEPARATELY FUNCTIONING PROTEINS.
-1			PMT: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE.
-1			SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN FAMILY.
-1			SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC			This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sdb.ch/announce/ or send an email to license@sdb-sw.ch).
CC			EMBL; U03642; AAB07599.1; .
DR	PIR;	A01209; TTB0B1.	
DR	HSSP;	P10646; IAD2.	
DR	INTERPRO;	IPR000566; .	
DR	INTERPRO;	IPR002223; .	
DR	INTERPRO;	IPR002345; .	
DR	PRAM;	PF00014; Kunitz_Bpti; 2.	
DR	PRAM;	PF00061; Lipocalin; 1.	
DR	PRINTS;	PR00179; LIPOCALIN.	
DR	PRINTS;	PR00759; BASICPLASE.	
DR	PROSITE;	PS00280; BPTI_KUNITZ_1; 2.	
DR	PROSITE;	PS50279; BPTI_KUNITZ_2; 2.	
DR	PROSITE;	PS00213; LIPOCALIN; 1.	
KW	Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat; Lipocalin.		
FW	SIGNAL	1	19
FT	CHAIN	20	203
FT	CHAIN	206	352
FT			
BINDING		53	53
DOMAIN		227	282
DOMAIN		283	348
DISULFID		91	188
DISULFID		231	281
DISULFID		240	264
DISULFID		256	277
DISULFID		287	337
DISULFID		296	320
DISULFID		312	333
DISULFID		241	242
ACT_SITE			
ACT_SITE		297	298
CARBOHYD		115	115
CARBOHYD		223	223
CARBOHYD		250	250
CARBOHYD		209	209
CONFLICT		217	217
CONFLICT		268	268
CONFLICT		274	274
CONFLICT		298	299
CONFLICT		330	330
CONFLICT		346	346
CARBOHYD		18	18
SEQUENCE	352 AA; 39235 MW; ED3JC5OAZET0B19 CRC64;		

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Query Match      26.3%  Score 249.5; DB 1; Length 352;
Best Local Similarity 32.4%; Pred. No. 3.9e-16;
Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

OY      9  DFCVYSKVYGRCRASMPRWYNYVDGSCQLEFYGGCDGNSNNYXLYKKEGCIKKCAVTENA 68
          1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      229 DSGCLDYSGPCGLGFKRYEYNGTSMACETFFYGGGCMGNNGNNFSEKELQICRYV----- 284

OY      69  TGDIALSRNAADSSVSPAPRQDSEHSDSMFVEEYCTANAVTGPCRASPRWYFDVER 128
          1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      285 -----EACHLPIYVGCGRSYIQLMAFDAYK 303

OY      129 NSCNNFIYGGCGRGKNKYSRSEACMLRC 156
          1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      310 GKCYRFSYGGCGKGNKRYSEKECYC 337

RESULT 2
AAMP_MERUN STANDARD; PRT; 346 AA.
AC      062577; 062576;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      AAMP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
DE      TRYPSIN INHIBITOR LIGHT CHAIN (ITI-1C) (BKUNIN) (H1-30)].
DE      AAMP OR ITIL.
OS      Meriones unguiculatus (Mongolian Jird).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC      Meriones.
RN      (1)
RN      SEQUENCE FROM N.A.
RC      TISSUE=LIVER;
RC      MEDLINE=95110820; Pubmed=7529051;
RA      Ide H., Itoh H., Nawa Y.;
RT      Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
RT      Mongolian gerbil and Syrian golden hamster in comparison with man and
RT      other species.";
RL      Biochim. Biophys. Acta 1209:286-292(1994).
CC      -1- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC      FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC      APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC      AND ALBUMIN (BY SIMILARITY).
CC      -1- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC      URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC      ELASTASE (BY SIMILARITY).
CC      -1- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC      SEPARATELY FUNCTIONING PROTEINS.
CC      -1- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE (BY
CC      SIMILARITY).
CC      -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC      FAMILY.
CC      -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC      FAMILY OF INHIBITORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL, D31813; BA06600.1; -
CC      DSSP, P10646; IADZ.
CC      INTERPRO: IPR000566; -
CC      INTERPRO: IPR002223; -
CC      INTERPRO: IPR002345; -
CC      Pfam, PF00014; Kunitz_BPTI; 2.
CC      Pfam, PF00061; lipocalin; 1.

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DR PRINTS: PR00179; LIPOCALIN.
DR PRINTS: PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
LIPOCALIN.
FT SIGNAL 1 19
FT CHAIN 20 202
FT CHAIN 205 346
FT DOMAIN 226 281
FT DOMAIN 282 345
FT BINDING 52 52
FT DISULFID 90 187
FT DISULFID 230 280
FT DISULFID 239 263
FT DISULFID 255 276
FT DISULFID 286 336
FT DISULFID 295 319
FT DISULFID 311 332
FT CARBOHYD 114 114
FT CARBOHYD 249 249
FT ACT_SITE 240 241
FT ACT_SITE 296 297
FT ACT_SITE 297
SQ SEQUENCE 346 AA; 38643 MW; F1A46381091BD5F CRC64;

Query Match
Best Local Similarity 32.4%; Score 247.5; DB 1; Length 346;
Matches 48; Conservative 15; Mismatches 46; Indels 39; Gaps 1;

QY 9 DFCIVSVYVGRCSMPRMWNTVDTSCQLFYVGGCDGNSNNYLTKECLKCAVTENA 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 228 DSCQLTYSRPGICRGEMERHNGTSMACEFFQYGGGLGNGNFISSKECLQTCRTVA-- 285
QY 69 TGDLATSRNAADSVSPAPRRODSEHSDMEYEEYCTANAVTGPCRSAPRWYDVER 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 286 -----CMLPYVGGPCRAVYIKLMDADAQ 308
QY 129 NSCNNTFYGGCGRGNKNSYSEACMLRC 156
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 309 GKCIQFTYGGCGKNGKNTFSEKECKEYC 336

RESULT 3
FPI_RAT STANDARD: PRT: 302 AA.
AC 002445;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-
DE ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR)
DE (EPI).
GN TFPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=92348361; PubMed=1639767;
RA Enjoji K.-I., Enli M., Mukai T., Kato H.;
RT "CDNA cloning and expression of rat tissue factor pathway inhibitor
RT (TFPI).";
RL J. Biochem. 111:681-687(1992).
-1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC WAY, INHIBITS VII(A)/TISSE FACTOR ACTIVITY, PREVIOUSLY BY FORMING
CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC ANTIHOMOBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC LIPOPROTEINS IN PLASMA.

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CC CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN HEART, LUNG, KIDNEY, AND
CC CC AORTIC ENDOTHELIAL CELLS.
CC CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC CC HIGHLY SIMILAR TO TFPI2.
-----
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CC CC or send an email to license@isb-sib.ch).
-----
DR EMBL; D10926; BAA01724.1; -.
DR PIR; JX0213; TIRTKG.
DR HSSP; P10646; 1TFX.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal.
FT SIGNAL 1 28
FT CHAIN 29 302
FT CHAIN 53 103
FT DOMAIN 124 174
FT DOMAIN 222 272
FT DISULFID 53 103
FT DISULFID 62 86
FT DISULFID 78 99
FT ACT_SITE 63 64
FT ACT_SITE 124 174
FT DISULFID 133 157
FT DISULFID 149 170
FT ACT_SITE 134 135
FT DISULFID 222 272
FT DISULFID 231 255
FT DISULFID 247 268
FT ACT_SITE 232 233
FT CARBOHYD 144 144
FT CARBOHYD 251 251
FT CARBOHYD 261 261
SQ SEQUENCE 302 AA; 34554 MW; F9AB82130A24A59F CRC64;

Query Match
Best Local Similarity 34.0%; Score 246.5; DB 1; Length 302;
Matches 54; Conservative 21; Mismatches 65; Indels 19; Gaps 3;

QY 9 DFCIVSVYVGRCSMPRMWNTVDTSCQLFYVGGCDGNSNNYLTKECLKCA-TYTEN 67
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 122 DFCLEEDPGLCRGFMTREYVNNQSKQCFKYGCGGCGNSNFFELTDCRNTCDPVNEY 181
QY 68 ATGDLATSR-----NAADSVSPAPRRODSEHSDMEYEEYCTANAVTGPCRA 117
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 182 QKGDYVNTQITVDRITVNNVVIPQATKAPSDMDYDPS-----WCLEPADSGICKA 233
QY 118 SFRPWYDVERNSCNNTFYGGCGRGNKNSYSEACMLRC 156
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 234 SEKRFYTPAIGRCROFNTYTCGCGNNNNFTTKQDCNRAC 272

RESULT 4
IATR SHEEP STANDARD: PRT: 123 AA.
ID IATR SHEEP
AC P13371;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)

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[illegible]

RESULT 5

ID	AMBP_HUMAN	STANDARD;	PRT;	352 AA.
AC	P02760; P02759; P00977;			
DI	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA-TRYPsin INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNININ) (HI-30)].			
DE	TRYPsin INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNININ) (HI-30)].			
DE	AMBP OR ITIL OR HCP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	(1)			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE-9121454; PubMed-1708673;			
RT	Vetr H., Gebhard W.;			
RL	"Structure of the human alpha 1-microglobulin-dikunin gene.";			
RN	Biol. Chem. Hoppe-Seyler 371:1185-1196(1990).			
RP	(2)			
RC	SEQUENCE FROM N.A.			
RA	TISSE-LIVER;			
RX	MEDLINE-87040757; PubMed-2430261;			
RT	Kameyager J.F., Polazzi J.O., Kottick M.P.;			
RL	"The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-trypsin inhibitor also encodes alpha-1-microglobulin (protein HC)."			
RT	Nucleic Acids Res. 14:7839-7850(1986).			
RN	(3)			
RX	SEQUENCE FROM N.A.			
RC	TISSE-LIVER;			
RX	MEDLINE-90336621; PubMed-1696200;			
RA	Diarré-Mehrour M., Bourguignon J., Seshou R., Saller J.P.,			
RT	Leveillard F., Martin J.P.;			
RL	"Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene.";			
RT	Eur. J. Biochem. 191:131-139(1990).			
RN	(4)			
RX	SEQUENCE OF 1-220 FROM N.A.			
RA	MEDLINE-86312901; PubMed-2428011;			
RT	Trebbin C., Corse E.;			
RL	"Sequence of a full length cDNA coding for human protein HC (alpha 1 microglobulin)."			
RT	Nucleic Acids Res. 14:6340-6340(1986).			
RN	(5)			
RX	SEQUENCE OF 20-202 (INDIVIDUAL WITH TUBULAR PROTEINURIA).			
RA	MEDLINE-84126849; PubMed-6198962;			
RT	Lopez C., Grubb A.O., Mendez E.;			
RL	"The complete amino acid sequence of human complex-forming glycoprotein heterogeneous in charge (protein HC) from one individual.";			
RT	Arch. Biochem. Biophys. 228:544-554(1984).			
RN	(6)			
RX	SEQUENCE OF 20-198 (VARIANT).			
RA	Lopez C., Grubb A.O., Mendez E.;			
RT	"Human protein HC displays variability in its carboxyl-terminal amino acid sequence.";			
RL	FEBS Lett. 144:349-353(1982).			
RN	(7)			
RX	SEQUENCE OF 20-198 (PATIENTS WITH TUBULAR PROTEINURIA).			
RA	MEDLINE-81184038; PubMed-6164372;			
RT	Takagi T., Takagi K., Kawai T.;			
RL	"Complete amino acid sequence of human alpha 1-microglobulin.";			
RN	Biochem. Biophys. Res. Commun. 98:997-1001(1981).			
RN	(8)			
RX	SEQUENCE OF 206-350.			
RA	MEDLINE-85225968; PubMed-2408638;			
RT	Reisiger P., Hochstrasser K., Albrecht G.J., Lempert K., Saller J.P.;			
RL	"Human inter-alpha-trypsin inhibitor: localization of the knits of domains in the N-terminal part of the molecule and their release.";			
RT	trypsin-like proteinase.";			
RL	Biol. Chem. Hoppe-Seyler 366:479-483(1985).			

```

CC CC      IN ITS SEQUENCE.
CC CC      -1- SUBUNIT: INTER-ALPHA-TYPEPSIN INHIBITOR CONSIST OF A LIGHT CHAIN
CC CC      AND AN HEAVY CHAIN. THERE ARE THREE DIFFERENT HEAVY CHAINS.
CC CC      -1- PPM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC CC      SEPARATELY FUNCTIONING PROTEINS.
CC CC      -1- PPM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE.
CC CC      -1- PPM: ADDITION OF GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, ALLOWS
CC CC      CROSS-LINKING BETWEEN THE DIFFERENT COMPONENTS.
CC CC      -1- MISCELLANEOUS: IN VITRO, THE FIRST TWELVE RESIDUES OF THE AMINO
CC CC      END OF THE INHIBITOR APPEAR TO HAVE A REACTIVE SITE CAPABLE OF
CC CC      INHIBITING THE ACTIVITY OF A NUMBER OF ENZYMES. ITS IN VIVO
CC CC      FUNCTION IS NOT KNOWN.
CC CC      -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC CC      FAMILY.
CC CC      -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC CC      FAMILY OF INHIBITORS.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC CC      at the European Bioinformatics Institute. There are no restrictions on
CC CC      use by non-profit institutions as long as its content is in its
CC CC      modified and this statement is not removed. Usage by and for commercial
CC CC      entities requires a license agreement (See http://www.isb-sib.ch/units
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL; X54816; CAA38585.1; -
CC CC      EMBL; X54817; CAA38585.1; JOINED.
CC CC      EMBL; X04225; CAA27803.1; -
CC CC      EMBL; M88249; AAA59196.1; -
CC CC      EMBL; M88165; AAA59196.1; JOINED.
CC CC      EMBL; M88243; AAA59196.1; JOINED.
CC CC      EMBL; M88244; AAA59196.1; JOINED.
CC CC      EMBL; M88246; AAA59196.1; JOINED.
CC CC      EMBL; M88247; AAA59196.1; JOINED.
CC CC      EMBL; X04494; CAA28182.1; -
CC CC      EMBL; X54817; CAA38586.1; -
CC CC      PIR; A03217; HCHD.
CC CC      PIR; A25303; A25303.
CC CC      PIR; S13433; S13433.
CC CC      PIR; S10717; S10717.
CC CC      PDB; 1BTK; 16-MAR-99.
CC CC      DR SWISS-2DPAGE; P02760; HUMAN.
CC CC      DR MIM; 176870; -
CC CC      DR INTERPRO; IPR000566; -
CC CC      DR INTERPRO; IPR002223; -
CC CC      DR INTERPRO; IPR002345; -
CC CC      DR PIRAM; PF000014; Kunitz_BPTI; 2.
CC CC      DR PIRAM; PF00061; Lipocalin; 1.
CC CC      DR PRINTS; PR00179; Lipocalin.
CC CC      DR PRINTS; PR00759; BASICPTASE.
CC CC      DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC CC      DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
CC CC      DR PROSITE; PS00213; Lipocalin; 1.
CC CC      KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
CC CC      Lipocalin; 3D-structure.

Query Match      25.8%; Score 244.5; DB 1; Length 352;
Best Local Similarity 32.4%; Pred. No. 1,1e-15;
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;

QY 9 DECLSVKVVGRRCASMPRMWYNTDSCQLFTVGGCDGNSNNYLTRECKLKCATVENA 68
Db 229 DSCQLGYSGPCKMGMTSRFYNGTSMACETFOYGGCGNGNNGNNEVTEKELQTCRTVA-- 286
QY 69 TGDLATSRNADSVSPAPRODSEHSDMEYEEYCTANATVGPRAFPFRYFEDVER 128
Db 287 -----CNLPYRGPCRAFIQTMAFDVAK 309
QY 129 NSCNNFYIGGCGNGNSYRSEACMLRC 156
Db 310 GKCVLFFPYGGCGNGNKKRYSEKREYEC 337

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QY	9	DELGVKVVGRCSRMRWYNTVDSQLEFVYGGCGGNSNNVLTREKJKCATVTEA	68
Db	214	DSQLEGGSPGCMGIRKRYFNSSMACELFHGGCGGNSNNVSEKELQTCVTEA	269
QY	69	TGDLATSRNADSVSPARRODSEHSSDMENEYECTANAVTGPCRASFPMRYEVDVER	128
Db	270	-----EACSLPIVSGRCRGPFQLMARDVAVQ	254
QY	129	NSCNNEFYGGCGRGNKNSYSEACMLRC	156
Db	295	GKCVLENNYGGCGGNGNFYSEKCKEYRC	322
RESULT	8		
IAFR_HORSE			
ID	IAFR_HORSE	STANDARD:	PRT; 123 AA.
AC	P04363;		
DT	20-MAR-1987 (Rel. 04, Created)		
DT	20-MAR-1987 (Rel. 04, Last sequence update)		
DT	01-APR-1990 (Rel. 14, Last annotation update)		
DE	INTER-ALPHA-TRYPSIN INHIBITOR (ITI) (HI-14) (INHIBITORY FRAGMENT OF ITI) (FRAGMENT)		
DE	EQUUS CABALLUS (HORSE).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
RN	[1]		
RP	SEQUENCE.		
RA	MEDLINE-85225967; PubMed-2408637;		
RA	Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;		
RT	"Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the trypsin-released inhibitors from horse and pig inter-alpha-trypsin inhibitors."		
RT	Biol. Chem. Hoppe-Seyler 366:473-478(1985).		
RL	-I- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS. WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE FIRST DOMAIN INTERACTS WEAKLY WITH PNN-GRANDULOCYTIC ELASTASE AND NOT AT ALL WITH PANCREATIC ELASTASE.		
CC	-I- MISCELLANEOUS: THE AMINO ACID AT POSITION P2; (17) APPEARS TO DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.		
CC	INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.		
CC	-I- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.		
DR	P1; A01210; TTHOI.		
DR	HSSP: P10646; IADZ.		
DR	INTERPRO: IPR002223; -		
DR	PFAM: PF00014; Kunitz_BPTI; 2.		
DR	PROSITE: PS00280; BPTI_KUNITZ_1; 2.		
DR	PROSITE: PS00279; BPTI_KUNITZ_2; 2.		
KW	Plasma; Glycoprotein; Serine protease inhibitor; Repeat.		
FT	DOMAIN	1	1
FT		56	56
FT		57	57
FT	DISULFID	5	53
FT		14	38
FT	DISULFID	30	51
FT		61	111
FT	DISULFID	70	94
FT		86	107
FT	DISULFID	15	16
FT	ACT_SITE		
FT		71	72
FT	CARBOHYD	24	24
FT	NON_TER	123	123
QO	SEQUENCE	123 AA; 13510 MW; CE1A912077441105 CRC64.	
		N-LINKED (GLCNAC. . .).	
		INHIBITORY SITE (P1) (CHYMOTRYPSIN.	
		ELASTASE).	
		INHIBITORY SITE (P1) (TRYPSIN).	

Query Match	25.5%;	Score 241.5;	DB 1;	Length 123,
Best Local Similarity	31.8%;	Pred. No. 6.6e-16;		

SEQ	CONFLICT SEQUENCE	142 349 AA;	142 3851 MW;	142 CRC64:
DR	PFAM: PF000014; Kunitz_BPT1; 2.			
DR	PFAM: PF000061; lipocalin; 1.			
DR	PRINTS: PR00179; LIPOCALIN.			
DR	PRINTS: PR00759; BASICPTASE.			
DR	PROSITE: PS00280; BPT1_KUNITZ_1; 2.			
DR	PROSITE: PS50279; BPT1_KUNITZ_2; 2.			
DR	PROSITE: PS00213; LIPOCALIN; 1.			
KW	Glycoprotein; Plasma; signal; Serine protease inhibitor; Repeat; lipocalin.			
FT	SIGNAL	1	19	BY SIMILARITY.
FT	CHAIN	20	202	ALPHA-1-MICROGLOBULIN.
FT	CHAIN	205	349	INTER-ALPHA-TRYPsin INHIBITOR LIGHT CHAIN.
FT				I.
FT	DOMAIN	226	281	II.
FT	DOMAIN	282	348	CHROMOPHORE (BY SIMILARITY).
FT	BINDING	52	52	BY SIMILARITY.
FT	DISULFID	90	187	BY SIMILARITY.
FT	DISULFID	230	280	BY SIMILARITY.
FT	DISULFID	239	253	BY SIMILARITY.
FT	DISULFID	255	276	BY SIMILARITY.
FT	DISULFID	286	336	BY SIMILARITY.
FT	DISULFID	295	319	BY SIMILARITY.
FT	DISULFID	311	332	BY SIMILARITY.
FT	CARBOHYD	114	114	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	233	233	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	ACT_SITE	240	241	INHIBITORY SITE (PI) (CHYMOTRYPSIN, ELASTASE) (BY SIMILARITY).
FT	ACT_SITE	296	297	INHIBITORY SITE (PI) (TRYPSIN) (BY SIMILARITY).
FT	ACT_SITE			G -> A (IN REF. 2).
FT	CONFLICT	142	142	
FT	SEQUENCE	349 AA;	3851 MW;	1B7B7DC0B824E01 CRC64;

RL J. Biochem. 115:708-714(1994).
 CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
 CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
 CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
 CC ANTIHROMBOCYTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
 CC LIPOPROTEINS IN PLASMA.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -1- PTM: O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 CC HIGHLY SIMILAR TO TFP2.
 CC -----
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 CC -----
 CC EMBL: S7337; AAB31955.1; -.
 CC INTERPRO: IPR002223; -.
 CC PFAM: PF00014; Kunitz_BPTI; 3.
 CC PRINTS: PR00759; BASICPTASE.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 3.
 CC PROSITE: PS00279; BPTI_KUNITZ_2; 3.
 CC Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
 CC Signal.
 CC FT SIGNAL 1 28 BY SIMILARITY.
 CC FT CHAIN 29 304 TISSUE FACTOR PATHWAY INHIBITOR.
 CC FT DOMAIN 54 104 BPTI/KUNITZ INHIBITOR 1.
 CC FT DOMAIN 125 175 BPTI/KUNITZ INHIBITOR 2.
 CC FT DOMAIN 125 175 (VIT(A)/TISSUE FACTOR BINDING SITE).
 CC FT DOMAIN 125 175 BPTI/KUNITZ INHIBITOR 3.
 CC FT DOMAIN 125 175 (FACTOR X(A) BINDING SITE).
 CC FT DOMAIN 125 175 BPTI/KUNITZ INHIBITOR 3.
 CC FT DISULFID 217 267 BY SIMILARITY.
 CC FT DISULFID 54 104 BY SIMILARITY.
 CC FT DISULFID 63 87 BY SIMILARITY.
 CC FT DISULFID 79 100 BY SIMILARITY.
 CC FT ACT_SITE 64 65 REACTIVE BOND (BY SIMILARITY).
 CC FT DISULFID 125 175 BY SIMILARITY.
 CC FT DISULFID 134 158 BY SIMILARITY.
 CC FT DISULFID 150 171 BY SIMILARITY.
 CC FT ACT_SITE 135 136 REACTIVE BOND (BY SIMILARITY).
 CC FT DISULFID 217 267 BY SIMILARITY.
 CC FT DISULFID 226 250 BY SIMILARITY.
 CC FT DISULFID 242 263 BY SIMILARITY.
 CC FT ACT_SITE 227 228 REACTIVE BOND (BY SIMILARITY).
 CC FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 304 AA; 35085 MW; 5613B3FF1628280 CRC64;

Query Match 24.9%; Score 236.5; DB 1; Length 304;
 Best Local Similarity 34.9%; Pred. No. 5.4e-15;
 Matches 53; Conservative 24; Mismatches 64; Indels 11; Gaps 4;

QY 9 DEFLVSKVGRGRASMPRMWYNTDGSQQLFYGGCDGNSNNYLTKEELKCAATYENA 68
 DB 123 DFCLEEDDPGICRGYITRYFYNNQSKOCERFKYGGCLNMNNFETLECKNCC--EDGL 179
 QY 69 TG----DLATSRNAADSVSPAPRROSEDSMDKFNTEYETAANVGPCCASPPRWTF 124
 DB 180 NGQVDVNGYGTQLNANVNS--QTP--QSTKVPSEFFHGHPSCWCLADPADRLCANENRFY 235
 QY 125 DYERNSCNFFIYGGCGRGNKNSYRSEACMLRC 156
 DB 236 NSYIGKCRPFKYGCGGCGNENNFISKECLTRAC 267
 RESULT 11
 AMBP_MESAU STANDARD; PRT; 349 AA.
 AC Q60559; Q60558;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE AMBP PROTEIN PRECURSOR (CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
 DE TRYPsin INHIBITOR LIGHT CHAIN (ITI-IC) (BIKUNIN) (HI-30)).
 GN AMBP OR ITIL.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=95110820; PubMed=7529051;
 RA Ide H., Itoh H., Nawa Y.;
 RT "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
 RT Mongolian gerbil and Syrian golden hamster in comparison with man and
 RT other species.";
 RL Blochim. Biophys. Acta 1209:286-292(1994).
 CC -1- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
 CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
 CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH TGA
 CC AND ALBUMIN (BY SIMILARITY).
 CC -1- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND
 CC URINE, INHIBITS TRYPsin, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
 CC ELASTASE (BY SIMILARITY).
 CC -1- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
 CC SEPARATELY FUNCTIONING PROTEINS.
 CC -1- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE LIPOCALIN
 CC FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE BPTI/KUNITZ
 CC FAMILY OF INHIBITORS.
 CC -----
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 CC tion between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D31814; BAA06601.1; -.
 CC HSSP: P10646; ITFX.
 CC DR INTERPRO: IPR000566; -.
 CC DR INTERPRO: IPR002223; -.
 CC DR INTERPRO: IPR002345; -.
 CC DR PFAM: PF00014; Kunitz_BPTI; 2.
 CC DR PFAM: PF00061; Lipocalin; 1.
 CC DR PRINTS: PR00759; BASICPTASE.
 CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
 CC DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
 CC DR PROSITE: PS00213; LIPOCALIN; 1.
 CC KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
 CC Lipocalin.
 CC FT SIGNAL 1 19 BY SIMILARITY.
 CC FT CHAIN 20 202 ALPHA-1-MICROGLOBULIN.
 CC FT CHAIN 205 349 INTER-ALPHA-TRYPsin INHIBITOR LIGHT
 CC CHAIN.
 CC FT DOMAIN 226 281 I.
 CC FT DOMAIN 282 348 II.
 CC FT BINDING 52 52 CHROMOPHORE (BY SIMILARITY).
 CC FT DISULFID 90 187 BY SIMILARITY.
 CC FT DISULFID 230 280 BY SIMILARITY.
 CC FT DISULFID 239 263 BY SIMILARITY.
 CC FT DISULFID 255 276 BY SIMILARITY.
 CC FT DISULFID 286 336 BY SIMILARITY.
 CC FT DISULFID 295 319 BY SIMILARITY.
 CC FT DISULFID 311 332 BY SIMILARITY.
 CC FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT ACT_SITE 240 241 INHIBITORY SITE (P1) (CHYMOTRYPSIN,
 FT ACT_SITE 296 297 ELASTASE) (BY SIMILARITY).
 FT INHIBITORY SITE (P1) (TRYPSIN) (BY
 FT SEQUENCE 349 AA; 38782 MW; 8C954584BDBE28 CRC64;
 SO
 Query Match 24.8%; Score 235.5; DB 1; Length 349;
 Best Local Similarity 31.1%; Pred. No. 7.8e-15;
 Matches 46; Conservative 17; Mismatches 46; Indels 39; Gaps 1;

QY 9 DECLVSKYVGRGRASMPRMWYNTDSCQLFYVGGDGNNSNYLTRECKLKCATVTEA 68
 DB 228 DSCQLVSYSGPCLGMETKTYTNGASMACETFFHYGGCLGNNGNNSSEKCIQTCTVA-- 285
 QY 69 TGDLATSRNADSVSPAFRRDSEDDHSDMFYEYECTANAVTGPCRASFPWYEDVER 128
 DB 286 -----CSLPYVQPCRAVYELMAFDAAQ 308

129 NSCNNFIYGGCGKGNKNSYSEACMLRC 156
 309 GKCVDFSYGGCKGNKGFYSEKCEKCYC 336

RESULT 12
 AAMP_MOUSE STANDARD; PRT; 349 AA.
 ID AAMP_MOUSE
 AC Q07456; Q61294;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE AAMP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
 DE TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)].
 GN AAMP OR ITIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-LIVER;
 RX MEDLINE-93363639; PubMed-7689339;
 RA Chan P., Salier J.P.;
 RT "Mouse alpha-1-microglobulin/Bikunin precursor: CDNA analysis, gene
 RT evolution and physical assignment of the gene next to the crossmucoid
 RT locus.";
 RL Biochim. Biophys. Acta 1174:195-200(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-LIVER;
 RX MEDLINE-95189774; PubMed-7533761;
 RA Itoh H., Ide H., Kataoka H., Tomita M., Yoshihara H., Nawa Y.;
 RT "CDNA sequencing of mouse alpha 1-microglobulin/inter-alpha-trypsin
 RT inhibitor light chain and its expression in acute inflammation.";
 RL J. Biochem. 116:767-772(1994).
 RN [3]
 RP SEQUENCE OF 128-349 FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-LIVER;
 RA Itoh H., Ide H., Yoshihara H., Nawa Y.;
 RT Submitted (Jan-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
 CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
 CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
 CC AND ALBUMIN (BY SIMILARITY).
 CC -1- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
 CC URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
 CC ELASTASE (BY SIMILARITY).
 CC -1- SUBUNIT: INTER-ALPHA-TRYPSIN INHIBITOR CONSIST OF A LIGHT CHAIN
 CC AND AN HEAVY CHAIN. THERE ARE THREE DIFFERENT HEAVY CHAINS.
 CC -1- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
 CC SEPARATELY FUNCTIONING PROTEINS.
 CC -1- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN

CC FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
 CC FAMILY OF INHIBITORS.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.slb.ch).
 CC -----
 CC EMBL: X68680; CAA48640.1; -;
 CC DR EMBL: D28812; BAA05973.1; -;
 CC DR HSP: P12111; 1KUN.
 CC DR MGD; MGI:88002; AAMP.
 CC DR INTERPRO: IPR000566; -;
 CC DR INTERPRO: IPR002223; -;
 CC DR INTERPRO: IPR002345; -;
 CC DR PRAM: PF00014; Kunitz_BPTI; 2.
 CC DR PRAM: PF00061; Lipocalin; 1.
 CC DR PRINTS: PR00179; LIPOCALIN.
 CC DR PRINTS: PR00759; BASICPTASE.
 CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
 CC DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
 CC DR PROSITE: PS00213; LIPOCALIN; 1.
 CC KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
 KW Lipocalin.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 202 ALPHA-1-MICROGLOBULIN.
 FT CHAIN 205 349 INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
 FT CHAIN
 FT DOMAIN 226 281 I.
 FT BINDING 282 348 I.
 FT BINDING 52 52 CHROMOPHORE (BY SIMILARITY).
 FT DISULFID 90 187 BY SIMILARITY.
 FT DISULFID 230 280 BY SIMILARITY.
 FT DISULFID 239 263 BY SIMILARITY.
 FT DISULFID 255 276 BY SIMILARITY.
 FT DISULFID 286 336 BY SIMILARITY.
 FT DISULFID 295 319 BY SIMILARITY.
 FT DISULFID 311 332 BY SIMILARITY.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 233 INHIBITORY SITE (P1) (CHYMOTRYPSIN).
 FT ACT_SITE 240 241 ELASTASE (BY SIMILARITY).
 FT ACT_SITE 296 297 INHIBITORY SITE (P1) (TRYPSIN) (BY
 FT ACT_SITE SIMILARITY).
 FT CONFLICT 65 65 Q -> S (IN REF. 2).
 FT SEQUENCE 349 AA; 39070 MW; CE4D9C7375DA80B CRC64;
 SO

Query Match 24.8%; Score 235.5; DB 1; Length 349;
 Best Local Similarity 29.7%; Pred. No. 7.8e-15;
 Matches 44; Conservative 18; Mismatches 47; Indels 39; Gaps 1;

QY 9 DECLVSKYVGRGRASMPRMWYNTDSCQLFYVGGDGNNSNYLTRECKLKCATVTEA 68
 DB 228 DSCQLVSYSGPCLGMETKTYTNGASMACETFFHYGGCLGNNGNNSSEKCIQTCTVA-- 285
 QY 69 TGDLATSRNADSVSPAFRRDSEDDHSDMFYEYECTANAVTGPCRASFPWYEDVER 128
 DB 286 -----CNLPYVQPCRAVYELMAFDAAQ 308

129 NSCNNFIYGGCGKGNKNSYSEACMLRC 156
 309 GKCVDFSYGGCKGNKGFYSEKCEKCYC 336

RESULT 13
 TPTI_HUMAN STANDARD; PRT; 304 AA.
 ID TPTI_HUMAN

AC p10646;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-
 DE ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR)
 GN TFPI OR TFPI OR LACI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88198127; PubMed=2452157;
 RA Wan T.-C., Kretzmer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.;
 RT Cloning and characterization of a cDNA coding for the lipoprotein-
 RT associated coagulation inhibitor shows that it consists of three
 RT tandem Kunitz-type inhibitory domains.";
 RT J. Biol. Chem. 263:6001-6004(1988).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA MEDLINE=91129227; PubMed=1993173;
 RA van der Logt C.P.E., Reitsma P.H., Bertina R.M.;
 RT "Intron-exon organization of the human gene coding for the
 RT lipoprotein-associated coagulation inhibitor: the factor xa dependent
 RT inhibitor of the extrinsic pathway of coagulation.";
 RT Biochemistry 30:1571-1577(1991).
 RL [3]
 RN SEQUENCE FROM N.A.
 RA MEDLINE=91161593; PubMed=2002045;
 RA Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A.,
 RA Likert K.M., Byers M.G., Shows T.B., Broze G.J. Jr.;
 RT "Structure of the human lipoprotein-associated coagulation inhibitor
 RT gene. Intron/exon gene organization and localization of the gene to
 RT chromosome 2.";
 RT J. Biol. Chem. 266:5036-5041(1991).
 RL [4]
 RN SEQUENCE FROM N.A.
 RA MEDLINE=89388722; PubMed=2781520;
 RA Girard T.J., Warren L.A., Novotny W.F., Bjelcek B.E., Miletich J.P.,
 RA Broze G.J. Jr.;
 RT "Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein
 RT associated coagulation inhibitor and expression of the encoded
 RT protein.";
 RT Thromb. Res. 55:37-50(1989).
 RL [5]
 RN SEQUENCE OF 29-50.
 RP MEDLINE=90036966; PubMed=2553722;
 RA Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;
 RT "Purification and characterization of the lipoprotein-associated
 RT coagulation inhibitor from human plasma.";
 RT J. Biol. Chem. 264:18832-18837(1989).
 RL [6]
 RN INHIBITORY SITES.
 RP MEDLINE=89181950; PubMed=2927510;
 RA Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,
 RA Miletich J.P., Broze G.J. Jr.;
 RT "Functional significance of the Kunitz-type inhibitory domains of
 RT lipoprotein-associated coagulation inhibitor.";
 RT Nature 338:518-520(1989).
 RL [7]
 RN CARBOHYDRATE-LINKAGE SITES.
 RP MEDLINE=96224851; PubMed=8639592;
 RA Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,
 RA Tsunawasa S., Kato H.;
 RT "Amino acid sequence and carbohydrate structure of a recombinant
 RT human tissue factor pathway inhibitor expressed in Chinese hamster
 RT ovary cells: one N- and two O-linked carbohydrate chains are located
 RT between Kunitz domains 2 and 3 and one N-linked carbohydrate chain is
 RT in Kunitz domain 2.";
 RL Biochemistry 35:6450-6459(1996).
 RN [8]
 RP REVIEW.

RX MEDLINE=91104709; PubMed=2271516;
 RA Broze G.J. Jr., Girard T.J., Novotny W.F.;
 RT "Regulation of coagulation by a multivalent Kunitz-type inhibitor.";
 RL Biochemistry 29:7539-7546(1990).
 RN [9]
 RP STRUCTURE BY NMR OF 121-182.
 RX MEDLINE=97342711; PubMed=9199408;
 RA Burgerling M.J., Orbons L.P., van der Doelen A., Mulders J.,
 RA Theunissen H.J., Grootehuis P.D., Bode W., Huber R., Stubbs M.T.;
 RT "The second Kunitz domain of human tissue factor pathway inhibitor:
 RT cloning, structure determination and interaction with factor Xa.";
 RL J. Mol. Biol. 269:395-407(1997).
 CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
 CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
 CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
 CC ANTIHEMORRHAGIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
 CC LIPOPROTEINS IN PLASMA.
 CC -1- TISSUE SPECIFICITY: MOSTLY IN ENDOTHELIAL CELLS.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -1- PTM: O-GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 CC HIGHLY SIMILAR TO TFPI2.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; J03225; AAA52022.1; -
 DR EMBL; M58650; AAA59480.1; -
 DR EMBL; M58644; AAA59480.1; JOINED.
 DR EMBL; M58645; AAA59480.1; JOINED.
 DR EMBL; M58646; AAA59480.1; JOINED.
 DR EMBL; M58647; AAA59480.1; JOINED.
 DR EMBL; M58648; AAA59480.1; JOINED.
 DR EMBL; M58649; AAA59480.1; JOINED.
 DR EMBL; M59493; AAA59526.1; JOINED.
 DR EMBL; M59494; AAA59526.1; JOINED.
 DR EMBL; M59495; AAA59526.1; JOINED.
 DR EMBL; M59496; AAA59526.1; JOINED.
 DR EMBL; M59497; AAA59526.1; JOINED.
 DR EMBL; M59498; AAA59526.1; JOINED.
 DR PIR; A28650; TIRUGK.
 DR PIR; A34315; A34315.
 DR PIR; A60433; A60433.
 DR PIR; S03903; S03903.
 DR PDB; 1ADZ; 25-FEB-98.
 DR PDB; 1TFX; 21-JAN-98.
 DR MIM; 152310; -
 DR INTERPRO: IPR002223; -
 DR PRAM: PF00014; Kunitz-BPTI; 3.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00289; BPTI_KUNITZ_1; 3.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 3.
 KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
 KM Signal; 3D-structure.
 FT SIGNAL 1 28
 FT CHAIN 29 304
 FT DOMAIN 54 104
 FT
 FT DOMAIN 125 175
 FT
 FT DOMAIN 217 267
 FT DISULFID 54 104
 FT DISULFID 63 87
 FT DISULFID 79 100
 FT ACT_SITE 64 65
 FT DISULFID 125 175
 FT DISULFID 134 158
 FT
 FT TISSUE FACTOR PATHWAY INHIBITOR.
 FT BPTI/KUNITZ INHIBITOR 1
 FT (VII(A)/TISSUE FACTOR BINDING SITE).
 FT BPTI/KUNITZ INHIBITOR 2
 FT (FACTOR X(A) BINDING SITE).
 FT BPTI/KUNITZ INHIBITOR 3.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT REACTIVE BOND (BY SIMILARITY).
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 150 177 BY SIMILARITY.
 FT ACT_SITE 135 136 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 217 267 BY SIMILARITY.
 FT DISULFID 226 250 BY SIMILARITY.
 FT DISULFID 242 263 BY SIMILARITY.
 FT ACT_SITE 227 228 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 202 202
 FT CARBOHYD 203 203
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 64 64 K->I: ABOLISHES INHIBITION OF VII(A)/TF.
 FT MUTAGEN 135 135 R->L: ABOLISHES INHIBITION OF X(A).
 FT MUTAGEN 227 227 R->L: ABOLISHES INHIBITION OF VII(A)/TF.
 FT SEQUENCE 304 AA: 35015 MW: 5281E32B758B44FE CRC64;

Query Match 24.6%; Score 233.5; DB 1; Length 304;
 Best Local Similarity 33.6%; Pred. No. 1e-14; Indels 11; Gaps 3;
 Matches 51; Conservative 26; Mismatches 64;

9 DCLVSKVYGRGRASMPRMWYNTDSCGLFYGGCGDGNNNYTLKECKLKCATVTEA 68
 123 DCFLEDEDEGICRGYTRFYNNOTKOCERFKYGGGLGMMNNETLECKNIC--EDGP 179
 69 TG----DLATSRNADSVSPAPRRDSEDDHSDMFNEYECTANAVTGPCRASFRWTF 124
 180 NGQVONVNGTQLVANVNSLTP---QSTKVPSLFEFFHGPSWCLTPADRGICRANENRFY 235

OY 125 DVERNSCNFTYGGCGRGNKSYSEECMLRC 156
 DB 236 NSVIGKCRPFKYSKCGGNGENNFYSKDECLNAC 267

RESULT 14
 ID TP22_HUMAN STANDARD; PRT; 235 AA.
 AC P48307;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR (TFPI-2) (PLACENTAL
 DE PROTEIN 5) (PP5).
 GN TFPI2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA TISSUE-PLACENTA;
 RA MEDLINE-95204397; PubMed-7896752;
 RA Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F.,
 Aoki I., Misugi K., Umeda M., Miyazaki K.,
 "cDNA cloning and mRNA expression of a serine proteinase inhibitor
 secreted by cancer cells: identification as placental protein 5 and
 tissue factor pathway inhibitor-2.";
 RT J. Biochem. 116:939-942(1994).
 RL [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE-PLACENTA;
 RA MEDLINE-94211862; PubMed-8159751;
 RA Sprechter C.A., Kistiel W., Mathewes S., Foster D.C.;
 "Molecular cloning, expression, and partial characterization of a
 second human tissue-factor-pathway inhibitor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:3353-3357(1994).
 RL [3]
 RP SEQUENCE FROM N.A.
 RP Maggi L.;
 RA Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
 RL [4]
 RP PARTIAL SEQUENCE OF 23-35; 47-53 AND 133-146.
 RP TISSUE-PLACENTA;
 RA MEDLINE-88106628; PubMed-3276332;
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;

RT "Purification and characterization of placental protein 5.";
 RL Biochem. Biophys. Res. Commun. 150:483-490(1988).
 RN [5]
 RP ERRATUM.
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;
 Biochem. Biophys. Res. Commun. 151:630-631(1988).
 RL Biochem. Biophys. Res. Commun. 151:630-631(1988).
 CC -1- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR,
 WEAKLY FACTOR XA, HAS NO EFFECT ON THROMBIN.
 CC -1- TISSUE SPECIFICITY: UMBILICAL VEIN ENDOTHELIAL CELLS, LIVER,
 PLACENTA, HEART, PANCREAS, AND MATERNAL SERUM AT ADVANCED
 PREGNANCY.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 CC HIGHLY SIMILAR TO TPFI.
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DR EMBL; D29992; BA06272.1; -
 DR EMBL; L27624; AAA20094.1; -
 DR EMBL; AC002076; AAB54049.1; -
 DR PIR; A34029; A34029.
 DR PIR; B34029; B34029.
 DR PIR; C34029; C34029.
 DR HSSP; P12111; IKNT.
 DR MIM; 600033; -
 DR INTERPRO; IPR002223; -
 DR PFAM; PF0014; Kunitz_BPTI; 3.
 DR PRINTS; PR00759; BASICPTASE.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
 DR Serine protease inhibitor; Glycoprotein; Repeat; signal;
 KW Blood coagulation.
 FT SIGNAL 1 22
 FT CHAIN 23
 FT DOMAIN 36 86
 FT DOMAIN 96 149
 FT DOMAIN 158 208
 FT DOMAIN 213 217
 FT DOMAIN 46 47
 FT ACT_SITE 107 108
 FT ACT_SITE 168 169
 FT ACT_SITE 36 86
 FT DISULFID 45 69
 FT DISULFID 61 82
 FT DISULFID 96 149
 FT DISULFID 106 130
 FT DISULFID 122 145
 FT DISULFID 158 208
 FT DISULFID 167 191
 FT DISULFID 183 204
 FT CARBOHYD 116 116
 FT CARBOHYD 170 170
 FT CONFLICT 23
 FT SEQUENCE 235 AA; 26934 MW; 975ABA5C53F7C65F CRC64;

Query Match 22.6%; Score 214.5; DB 1; Length 235;
 Best Local Similarity 25.9%; Pred. No. 4.4e-13;
 Matches 53; Conservative 31; Mismatches 66; Indels 55; Gaps 5;

9 DCLVSKVYGRGRASMPRMWYNTDSCGLFYGGCGDGNNNYTLKECKLKCATVTEA 68
 34 EICLPLDVGPCRALILYRYDRTYQSCRFYGGCGENANNFTWEGCDACWIEKVP 93
 62 ----ATYENATGDL-----ATSRNADSVSPS-----APR 60
 DB 94 KVCRLQVSDVDCSGSTKTEYFNLSMTCERFFSGGCHNRLENFPEATCMGFCAPEK 153

QY 90 QSDSDHSSDMFNEYCTANAVTGPCRASPRWYFVDERNSCNFTYGGCRGNKNSRSE 149
 DB 154 IPS-----FCYSPDEBLCASNVTRYNNPRYRCDAFTYGGGNDNNVSR 201
 QY 150 EACMLRCF-----RQGNPPPLGSK 170
 DB 202 EDCRRACAKAKKKKKMKPLRFASR 226

RESULT 15
 APP2_RAT
 ID APP2_RAT STANDARD: PRT: 765 AA.
 AC P15943;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AMYLOID-LIKE PROTEIN 2 PRECURSOR (SPERM MEMBRANE PROTEIN YW-II).
 RNP2.
 Rattus norvegicus (Rat).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 SEQUENCE OF 1-627 FROM N.A.
 RC STRAIN=WISTAR; TISSUE=BRAIN; AND HEART;
 RC MEDLINE=94368649; PubMed=8086458;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "Complete nucleoside and deduced amino acid sequence of rat amyloid
 RT protein precursor-like protein 2 (APP2/APPH): two amino acids length
 RT difference to human and murine homologues.";
 RL Biochim. Biophys. Acta 1219:167-170(1994).
 RN [2]
 RP SEQUENCE OF 575-765 FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=90207205; PubMed=1690887;
 RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
 RT "Characterization of cDNA encoding a human sperm membrane protein
 RT related to A4 amyloid protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHOWN HERE), B, C AND D;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS A PROTEASE INHIBITOR DOMAIN BELONGING TO
 CC THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC -----
 CC EMBL: X77934; CA54906.1; -;
 DR EMBL: M31322; AAA42352.1; -;
 DR PIR: A35981; A35981.
 DR HSSP: P05067; 1CA0.
 DR INTERPRO: IPR001868; -;
 DR INTERPRO: IPR002223; -;
 DR PFAM: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Transmembrane; Alternative splicing; Serine protease inhibitor;
 KW Signal; Glycoprotein.
 FT SIGNAL 1 29
 FT CHAIN 30 765
 FT DOMAIN 30 695
 FT TRANSMEM 696 718
 FT POTENTIAL.
 FT AMYLOID-LIKE PROTEIN 2.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.

FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 218 282 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 308 366 BPTI/KUNITZ INHIBITOR.
 FT ACT_SITE 322 323 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 312 362 BY SIMILARITY.
 FT DISULFID 321 345 BY SIMILARITY.
 FT DISULFID 337 358 BY SIMILARITY.
 FT DOMAIN 218 229 POLY-GLU.
 FT CARBOHYD 628 628 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT VARSPPLIC 311 365 MISSING (IN ISOFORM C AND ISOFORM D).
 FT VARSPPLIC 616 627 MISSING (IN ISOFORM B AND ISOFORM D).
 FT CONFLICT 575 577 DOF -> ETV (IN REF. 2).
 SQ SEQUENCE 765 AA; 86882 MM; CF5IFCCCE305A0CF CRC64;

Query Match 22.2%; Score 210; DB 1; Length 765;
 Best Local Similarity 27.5%; Pred. No. 4.3e-12;
 Matches 58; Conservative 22; Mismatches 55; Indels 76; Gaps 2;

QY 28 WYVYTDGSC-----QLFVYG-----GCDG-----NSNNYLRKE----- 56
 DB 166 WHTVVKEACLTGNTLYSGMLPCGYDQFHGTEYVCCPQTKVYDSDSTMSKEEEEEE 225
 QY 57 -----CLKRCATYVENATGDLATSRNAADSSVSPAPRQDSE-----DHSDMFY 102
 DB 226 DEDEDYALDKSEPTF---ADLEDFTAAADEDEDEEEEEEVEVEDRYYVDSFGK 282
 QY 103 EBY-----CTANAVTGPCRASPRWYFVDERNSCNFTY 135
 DB 283 DYNEENPEPSSDGTISDKREIAHDYKAVKQSEAMTGPCRAVPRWYFDLSGKCVRFY 302
 QY 137 GCGRGKNSYRSFEACLRFRQENPPL 167
 DB 343 GCGGGRNNFSESDYCAVC--RTMIPPTPL 371

Search completed: January 31, 2001, 15:05:07
 Job time: 119 sec


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RESULT 5
Q9W004 PRELIMINARY; PRT; 195 AA.
AC Q9W004:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2 SPLICE VARIANT 1.
GN HA12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=BALB/C;
MEDLINE=99160423; PubMed=10049781;
Itoh H., Kataoka H., Hamasuna R., Kitamura N., Kono M.,
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT Kunitz-type serine protease inhibitor domain is a predominant
RT product in mouse but not in human."
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
DR EMBL: AF099019; AAD22173.1; -.
DR HSSP: P05067; 1TAM.
DR INTERPRO: IPR002223; -.
DR PFAM: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PROSITE: PS00280; BPTI_KUNITZ; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 195 AA; 21736 MW; EF49C83AB4E3EDE0 CRC64;

Query Match
Best Local Similarity 40.2%; Score 381; DB 11; Length 195;
Pred. No. 1,7e-33;
Matches 69; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 64 VVENATGDLATSRNADSSVPSAPRRDSDHSDMFNYEYCTANAVTGPCRAAFPRMY 123
DB 34 VHEMTDDMARNNAGDSVLSVPRKOSAEIDLSAEIFNYEYCVPAKAVTGCRAAFPAMY 93
QY 124 FVERNSCNFIYGGCGNGNSYRSEACMLRCFROENPLPLGSK 170
DB 94 YDEKSCISFTYGGCGNGNNSILSDCAQKHCSGKOMHPPLPLGLK 140

RESULT 6
Q43278 PRELIMINARY; PRT; 513 AA.
AC Q43278:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=97197808; PubMed=9045658;
Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J.,
RA Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;
RT "Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
RT serine protease inhibitor."
RL J. Biol. Chem. 272:6370-6376(1997).
DR EMBL: AB000095; BAA25014.1; -.
DR HSSP: P31713; 1SHP.
DR INTERPRO: IPR002172; -.
DR INTERPRO: IPR002223; -.
DR PFAM: PF00014; Kunitz_BPTI; 2.
DR PFAM: PF00057; Idl_recept_a; 1.
DR PFAM: PF00057; Idl_recept_a; 1.

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DR PRINTS: PR00759; BASICPTASE.
DR PROSITE: PS00280; BPTI_KUNITZ; 2.
DR PROSITE: PS01209; IDIRA_1; 1.
DR PROSITE: PS50068; IDIRA_2; 1.
KW Glycoprotein; Serine protease inhibitor.
SQ SEQUENCE 513 AA; 56885 MW; D6E05F3A5885CDDC CRC64;

Query Match
Best Local Similarity 32.9%; Score 312; DB 4; Length 513;
Pred. No. 1,4e-25;
Matches 67; Conservative 24; Mismatches 71; Indels 38; Gaps 3;

QY 5 RSIHDFCLVSKYVGRCSRAMPKRWYNTVDTGSCQLFYGGCGDGSNNYLTRECKLKCAATV 7
DB 244 KQEDYCLASNNVGRGSGFPFRWYDPTDQICKSFYGGCLGKNNYLTREECILACRGV 273
QY 65 -----TENATGDLATSRNADSSVPSAPRRDSDHSDMFNYEYCTANAVTGPCRAAFPRMY 102
DB 304 QGPMERRHPVCSGTCQPFQFRCSNGCIDSFLECDTTPNCPPASDEACEKYSGFDEL 363
QY 103 EE-----YCTANAVTGPCRAAFPRMYEDVRNCSNFIYGGCGGKNNYSSEACML 154
DB 364 QIHPSPDKHCYVDLPDTGLCKESIPRWYNPSEHCARFTYGGCYGNKNFEEQCLE 423
QY 155 RC-----FROENPLPL 166
DB 424 SCRGISKVDFGLRREIRIP 443

RESULT 7
Q9R097 PRELIMINARY; PRT; 507 AA.
AC Q9R097:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 1.
GN SPINT1 OR HA11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=BALB/C;
Itoh H., Kataoka H., Kono M.;
RT "Mouse hepatocyte growth factor activator inhibitor type 1 (HA1-1).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF099018; AAF02490.1; -.
DR HSSP: P05067; 1TAM.
DR MGD: MGI:1338033; Spint1.
DR INTERPRO: IPR002172; -.
DR INTERPRO: IPR002223; -.
DR PFAM: PF00014; Kunitz_BPTI; 2.
DR PFAM: PF00057; Idl_recept_a; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PROSITE: PS00280; BPTI_KUNITZ; 2.
DR PROSITE: PS50068; IDIRA_2; 1.
SQ SEQUENCE 507 AA; 56676 MW; 20CB5DEDCFE46AA7 CRC64;

Query Match
Best Local Similarity 31.0%; Score 294; DB 11; Length 507;
Pred. No. 1,2e-23;
Matches 59; Conservative 23; Mismatches 66; Indels 30; Gaps 3;

QY 9 DFLCVSKYVGRCSRAMPKRWYNTVDTGSCQLFYGGCGDGSNNYLTRECKLKCAATV----- 64
DB 242 DYLASYKVGKRGSGFPFRWYDPTDQICKSFYGGCLGKNNYLTREECILACRGV 301
QY 65 -----TENATGDLATSRNADSSVPSAPRRDSDHSDMFNYEYCTANAVTGPCRAAFPRMY 102
DB 302 PKRHVYCSGCHATQFRCSNGCIDSFLECDTTPDCPDGSDATCEKYSYGFDELONTH 361

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DE THROMBOSPONDIN-LIKE PROTEIN (FRAGMENT).
 GN THRI.
 OS Haemochus contortus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Trichostrongylidae; Haemonchidae; Haemonchinae; Haemonchus.
 OX NCBI_TaxID=6289;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOREDUN;
 RA Newlands G.F.J., Skuce P.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF043121; AAB99830.1; .
 DR HSSP: P05067; ITAM
 DR INTERPRO: IPR002223; .
 DR PFAM: PF00014; Kunitz_BPTI; 6.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 6.
 DR Serine protease inhibitor.
 NON_TER 1
 SEQUENCE 972 AA; 105301 MW; 4465C6BE8DC19ED CRC64;

Query Match 27.1%; Score 256.5; DB 5; Length 972;
 Best Local Similarity 30.1%; Pred. No. 2,6e-19;
 Matches 47; Conservative 21; Mismatches 61; Indels 27; Gaps 1;
 OY 11 CLVSKVYGRASMPRMWYNTDSCQLFVYGGCDGNSNNYLTKECLKCAVTENATG 70
 DB 794 CHLPDVGCGSFDSPYEMATGSCVEFKYSGSGNANRFRASRECENTCV----- 845
 OY 71 DIATSRNADSSVPSAPRRDSEDSDFNFYEYCTANAVTGPCRASFPFRWYDVER 130
 DB 846 -----RHSEPHSDTTSHTGTSVDEKKEFGPCTNRATKMYNKKADGT 886
 OY 131 CNNEFYGGCGRNKNSYRSEECMLRCFRQENPPLP 166
 DB 887 CNRFHYGCGEGRNFRDNEQSCAKANHODACTLP 922

RESULT 11
 ID 09088 PRELIMINARY; PRT; 3198 AA.
 AC 09088;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE LACUNIN PRECURSOR.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Phryganea; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptysia;
 OC Spingidae; Spingidae; Spinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99457716; PubMed-10528409;
 RA Nardi J.B., Matos R., Walden K.K., Lampe D.J., Robertson H.M.;
 RT "Expression of lacunin, a large multidomain extracellular matrix
 RT protein, accompanies morphogenesis of epithelial monolayers in Manduca
 RT sexta."
 RL Insect Biochem. Mol. Biol. 29:883-897(1999).
 DR EMBL: AF078161; AAF04457.1; .
 DR HSSP: P12111; 2KNT.
 DR INTERPRO: IPR000884; .
 DR INTERPRO: IPR002221; .
 DR INTERPRO: IPR002223; .
 DR INTERPRO: IPR003006; .
 DR PFAM: PF00014; Kunitz_BPTI; 10.
 DR PFAM: PF00047; Ig; 2.
 DR PFAM: PF00095; Wap; 1.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 8.
 DR PROSITE: PS00317; 4_DISULFIDE_CORE; 1.
 KW Signal.

FT SIGNAL 1 21 POTENTIAL.
 SQ SEQUENCE 3198 AA; 349366 MW; AB4ACD459C0D9134 CRC64;
 Query Match 26.9%; Score 255; DB 5; Length 3198;
 Best Local Similarity 31.7%; Pred. No. 1.4e-18;
 Matches 51; Conservative 23; Mismatches 63; Indels 24; Gaps 3;
 OY 9 DFCIVSKVYGRASMPRMWYNTDSCQLFVYGGCDGNSNNYLTKECLKCAVTENA 68
 DB 2133 DLCTLPALIDCADYREKRWYDTRKSCQRFYTGCGAGNNGNPFATQAECEGRC----- 2185
 OY 69 TGLDLSRNADSSVPSAPRRDSEDSDFNFYEYCTANAVTGPCRASFPFRWYDVER 128
 DB 2186 -----SEAKITTVR--PTEAHP-----LTMCMEKDPGPGCTDTRWYDYKL 2228
 OY 129 NSCNFYGGCGRNKNSYRSEECMLRCFRQENPPLPUGS 169
 DB 2229 GKCVTFEYGGCGGNRNNPFTEYCYQYCGTADICQLPMRS 2269

RESULT 12
 ID 093424 PRELIMINARY; PRT; 287 AA.
 AC 093424;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE HYPOTHETICAL 33.1 KDA PROTEIN.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Gracey A.Y.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF008648; AAC19410.1; .
 DR HSSP: P31713; 1SHP.
 DR INTERPRO: IPR002223; .
 DR PFAM: PF00014; Kunitz_BPTI; 3.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 3.
 KW Hypothetical protein; Serine protease inhibitor.
 SQ SEQUENCE 287 AA; 33093 MW; DF69B3D76718115E CRC64;

Query Match 26.6%; Score 252; DB 13; Length 287;
 Best Local Similarity 30.9%; Pred. No. 2.1e-19;
 Matches 50; Conservative 19; Mismatches 53; Indels 40; Gaps 3;
 OY 8 HDCLIVSKVYGRASMPRMWYNTDSCQLFVYGGCDGNSNNYLTKECLKCAVTEN 67
 DB 39 HHSCLAKDGKPGKALKDRYFDLDRGRCSEFYGGCGQGNENFETLQCEKMKIV---- 94
 OY 68 ATGDLATSRNADSSVPSAPRRDSEDSDFNFYEYCTANAVTGPCRASFPFRWYDVE 127
 DB 95 -----KDKKSP-----CQLDDEPQCGGLVRYEYDFK 122
 OY 128 NSCNFYGGCGRNKNSYRSEECMLRCF---RQENPPL 165
 DB 123 SQCKRFFYGGCGGNANRNNFKIKRCHERCLPALNNERNAPL 164

RESULT 13
 ID 076840 PRELIMINARY; PRT; 2167 AA.
 AC 076840; Q22911;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

QY 121 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 170
 DB 148 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 197

RESULT 2

ID 000271 PRELIMINARY; PRT; 252 AA.

AC 000271; 1
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE BIKININ.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RS TISSUE=PLACENTA;
 MEDLINE=9727372; PubMed=9115294;
 MA Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
 RA Tamburini P.P.;
 RT "Identification and cloning of human placental bikinin, a novel serine
 RT protease inhibitor containing two Kunitz domains.";
 RL J. Biol. Chem. 272:12202-12208(1997).
 DR HSSP; P05067; ITAM
 DR HSSP; P05067; ITAM
 DR INTERPRO: IPR002223;
 DR PFAM: PF00014; Kunitz_BPTI; 2.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 2.
 KW Serine protease inhibitor.
 SQ SEQUENCE 252 AA; 28228 MW; A7D3360C0CEBAC2B CRC64;

Query Match 100.0%; Score 948; DB 4; Length 252;
 Best Local Similarity 100.0%; Pred. No. 1.7e-94;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADDRESSHDFCLVSKVYVRCRASPMPRMWNTYDSCQLFYVGGCDGNSNYLTKECLCK 60
 DB 28 ADDRESSHDFCLVSKVYVRCRASPMPRMWNTYDSCQLFYVGGCDGNSNYLTKECLCK 87
 QY 61 CATVTENATGDLATSRNADSSVPSAPRRDSEDSHSDMFNVEEYCTANAVTGCRASFP 120
 DB 88 CATVTENATGDLATSRNADSSVPSAPRRDSEDSHSDMFNVEEYCTANAVTGCRASFP 147
 DB 121 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 170
 DB 148 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 197

RESULT 3
 ID 014895 PRELIMINARY; PRT; 252 AA.
 AC 014895;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE KUNITZ-TYPE PROTEASE INHIBITOR.
 GN Kop.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RS TISSUE=PANCREATIC CANCER;
 MA Mueller-Pillasch F., Wallirapp C., Bartels K., Varga G., Friess H.,
 RA Buechler M., Adler G., Gress T.M.;
 RL Biochem. Biophys. Acta 0:0-0(1997).
 DR EMBL; AF027205; AAB84031.1; -.

DR HSSP; P05067; ITAM.
 DR INTERPRO: IPR002223;
 DR PFAM: PF00014; Kunitz_BPTI; 2.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 2.
 KW Serine protease inhibitor.
 SQ SEQUENCE 252 AA; 28231 MW; B21593466413841E CRC64;

Query Match 99.7%; Score 945; DB 4; Length 252;
 Best Local Similarity 99.4%; Pred. No. 3.3e-94;

Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADDRESSHDFCLVSKVYVRCRASPMPRMWNTYDSCQLFYVGGCDGNSNYLTKECLCK 60
 DB 28 ADDRESSHDFCLVSKVYVRCRASPMPRMWNTYDSCQLFYVGGCDGNSNYLTKECLCK 87
 QY 61 CATVTENATGDLATSRNADSSVPSAPRRDSEDSHSDMFNVEEYCTANAVTGCRASFP 120
 DB 88 CATVTENATGDLATSRNADSSVPSAPRRDSEDSHSDMFNVEEYCTANAVTGCRASFP 147
 QY 121 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 170
 DB 148 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 197

RESULT 4

ID 09WU03 PRELIMINARY; PRT; 252 AA.

AC 09WU03;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.
 GN HA12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RS STRAIN=BA1B/C;
 MEDLINE=99160423; PubMed=10049781;
 RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
 RT Hepatocyte growth factor activator inhibitor type 2 lacking the first
 RT Kunitz-type serine protease inhibitor domain is a predominant
 RT product in mouse but not in human.";
 RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
 DR HSSP; P05067; ITAM.
 DR HSSP; P05067; ITAM.
 DR INTERPRO: IPR002223;
 DR PFAM: PF00014; Kunitz_BPTI; 2.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 2.
 KW Serine protease inhibitor.
 SQ SEQUENCE 252 AA; 27914 MW; B2PF4B86924D4F8F CRC64;

Query Match 69.9%; Score 663; DB 11; Length 252;
 Best Local Similarity 68.2%; Pred. No. 9e-64;

Matches 116; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

QY 1 ADDRESSHDFCLVSKVYVRCRASPMPRMWNTYDSCQLFYVGGCDGNSNYLTKECLCK 60
 DB 28 ASRELVDHESGVSKVYVRCRASPMPRMWNTYDSCQLFYVGGCDGNSNYLTKECLCK 87
 QY 61 CATVTENATGDLATSRNADSSVPSAPRRDSEDSHSDMFNVEEYCTANAVTGCRASFP 120
 DB 88 CAGVTENTTDMARNRNDSSVLSVPRKQSAEDLSAIFNVEEYCPKAVATGCRASFP 147
 QY 121 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 170
 DB 148 RMYEDVERNSCNNTFYGGCRGNKNSYSEACMLRCFROQENPPLPGSK 197

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:02:44 ; Search time 23.18 Seconds
(without alignments)
859,592 Million cell updates/sec

Title: US-09-441-654A-1

Perfect score: 948
Sequence: 1 ADREKSHDFCLNKNVGRG.....ACMLRCFRQENPPLFLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: SP-archaea:*

2: SP-bacteria:*

3: SP-fungi:*

4: SP-human:*

5: SP-invertebrate:*

6: SP-mammal:*

7: SP-mmc:*

8: SP-organism:*

9: SP-phage:*

10: SP-plant:*

11: SP-rodent:*

12: SP-virus:*

13: SP-vertebrate:*

14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	252	4	043291 homo sapien
2	948	100.0	252	4	000271 homo sapien
3	945	99.7	252	4	014895 mus musculu
4	663	69.9	252	11	09WU03 mus musculu
5	381	40.2	195	11	09WU04 mus musculu
6	312	32.9	513	4	043278 mus musculu
7	294	31.0	507	11	09R097 mus musculu
8	259.5	27.4	306	11	054819 mus musculu
9	259	27.3	2230	5	09VAN4 mus musculu
10	256.5	27.1	972	5	044938 mus musculu
11	255	26.9	3198	5	09U868 mus musculu
12	252	26.6	287	13	093424 cyprinus ca
13	250.5	26.4	2167	5	076840 caenorhabd
14	244.5	25.8	151	4	078491 homo sapien
15	240	25.3	2225	5	045881 caenorhabd
16	239.5	25.3	396	6	028874 canis famli
17	235.5	24.8	144	11	090W87 mesocricetu
18	233.5	24.6	352	11	070160 cavia porce
19	228	24.1	251	4	095103 homo sapien

20	227.5	24.0	246	11	092208 mus musculu
21	222	23.4	1043	5	017644 caenorhabd
22	219.5	23.2	342	13	P70004 xenopus lae
23	219	23.1	922	5	021418 caenorhabd
24	209	22.0	1743	5	09XW85 caenorhabd
25	208	21.9	751	11	060709 mus musculu
26	208	21.6	763	11	061482 mus musculu
27	204.5	21.6	230	11	035536 mus musculu
28	200	21.1	523	4	014594 mus musculu
29	200	21.0	1599	5	009983 mus musculu
30	199	21.0	1522	5	022685 caenorhabd
31	198	20.9	1195	5	09N343 caenorhabd
32	195	20.6	1391	5	019021 caenorhabd
33	194	20.5	1297	5	09U350 caenorhabd
34	193	20.4	1474	5	062504 caenorhabd
35	186.5	19.7	747	13	091963 xenopus lae
36	186	19.6	484	4	013793 homo sapien
37	186	19.6	547	4	013764 homo sapien
38	186	19.6	770	6	09T010 sus scrofa
39	185.5	19.6	1203	5	045916 caenorhabd
40	183	19.3	160	11	09Q278 caenorhabd
41	178	18.8	1965	5	061893 caenorhabd
42	177	18.7	59	5	09TWE8 caenorhabd
43	174.5	18.4	692	5	045101 caenorhabd
44	174.5	18.4	780	13	073683 tetracodon
45	173	18.2	58	5	09TWE9 anemonia su

ALIGNMENTS

RESULT	ID	SEQUENCE FROM N.A.	PRELIMINARY	PRT	252 AA.
043291	043291	01-JUN-1998 (TREMBLrel. 06, Created)			
AC	043291	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-JUN-1998	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DT	01-OCT-2000	HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.			
DE	HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.	Homo sapiens (Human).			
OC	Homo sapiens (Human).	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI_TaxID=9606;			
OX	NCBI_TaxID=9606;	[1]			
RN	[1]	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.	MEDLINE=98010584; PubMed=9346890;			
RX	MEDLINE=98010584; PubMed=9346890;	Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denta K.,			
RA	Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denta K.,	Kitamura N.;			
RA	Kitamura N.;	"Purification and cloning of hepatocyte growth factor activator			
RT	"Purification and cloning of hepatocyte growth factor activator	inhibitor type 2, a Kunitz-type serine protease inhibitor.";			
RL	inhibitor type 2, a Kunitz-type serine protease inhibitor.";	J. Biol. Chem. 272:27558-27564(1997).			
DR	J. Biol. Chem. 272:27558-27564(1997).	EMBL; AB006534; BAA25024.1; -			
DR	EMBL; AB006534; BAA25024.1; -	HSSP; P05067; ITAM.			
DR	HSSP; P05067; ITAM.	INTERPRO: IPR002223; -			
DR	INTERPRO: IPR002223; -	PFAM: PF00014; Kunitz_BPTI; 2.			
DR	PFAM: PF00014; Kunitz_BPTI; 2.	PRINTS: PR00759; BASICPTASE.			
DR	PRINTS: PR00759; BASICPTASE.	PROSITE: PS00280; BPTI_KUNITZ; 2.			
KW	PROSITE: PS00280; BPTI_KUNITZ; 2.	Serine protease inhibitor.			
SQ	Serine protease inhibitor.	SEQUENCE 252 AA; 28169 MW; F7D3D834ED631DF0 CRC64;			

Query Match 100.0%; Score 948; DB 4; Length 252;
Best local similarity 100.0%; Pred. No. 1.7e-94;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ADREKSHDFCLNKNVGRGASPRWVYNTDSCOLFYYGGGDSNNYLKEECLKK 60
QY	1	ADREKSHDFCLNKNVGRGASPRWVYNTDSCOLFYYGGGDSNNYLKEECLKK 60
DB	28	ADREKSHDFCLNKNVGRGASPRWVYNTDSCOLFYYGGGDSNNYLKEECLKK 87
QY	61	CATYENATGDIATSRNADSVSPAPRRDSEHSSDMRYEYCTANATGCRASFP 120
QY	61	CATYENATGDIATSRNADSVSPAPRRDSEHSSDMRYEYCTANATGCRASFP 120
DB	88	CATYENATGDIATSRNADSVSPAPRRDSEHSSDMRYEYCTANATGCRASFP 147

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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:02:39 ; Search time 16.59 seconds

(without alignments)
350,388 Million cell updates/sec

Title: US-09-441-654a-1

Sequence: 1 ADRRSIHDFCLVSKVVGRC.....ACMURCFROENPLPLGSK 170

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

268485 seqs, 34193795 residues

Database: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT.*
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19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	170	W30041	Human placental bi
2	948	100.0	179	W30053	Human placental bi
3	948	100.0	197	W30043	Human placental bi
4	948	100.0	213	W30042	Human placental bi
5	948	100.0	225	W30046	Human placental bi
6	948	100.0	235	W30060	Human placental bi
7	948	100.0	240	W30045	Human placental bi
8	948	100.0	248	W30044	Human placental bi
9	948	100.0	252	W30040	Human placental bi
10	948	100.0	252	W30040	Human placental bi
11	948	100.0	252	W30040	Human placental bi
12	859	90.6	153	W30051	Human placental bi

13	819	86.4	146	W30052	Human placental bi
14	750	79.1	170	W30061	Human placental bi
15	501	52.8	92	W30054	Human placental bi
16	488	51.5	130	W30062	Human placental bi
17	487	51.4	169	W30063	Human placental bi
18	337	35.5	58	W30049	Human placental bi
19	334	35.2	58	W30049	Human placental bi
20	312	32.9	513	W30047	Human placental bi
21	312	32.9	513	W30047	Human placental bi
22	297	31.3	51	W30048	Human placental bi
23	297	31.3	51	W30048	Human placental bi
24	281	29.6	128	W30050	Human placental bi
25	277	29.2	128	W30050	Human placental bi
26	276	29.1	128	W30050	Human placental bi
27	274	28.9	128	W30050	Human placental bi
28	273	28.8	128	W30050	Human placental bi
29	272.5	28.7	124	W30050	Human placental bi
30	272.5	28.7	124	W30050	Human placental bi
31	272	28.7	128	W30050	Human placental bi
32	272	28.7	128	W30050	Human placental bi
33	272	28.7	128	W30050	Human placental bi
34	271.5	28.6	124	W30050	Human placental bi
35	271.5	28.6	144	W30050	Human placental bi
36	271.5	28.6	145	W30050	Human placental bi
37	271.5	28.6	145	W30050	Human placental bi
38	267	28.2	128	W30050	Human placental bi
39	267	28.2	128	W30050	Human placental bi
40	266.5	28.1	128	W30050	Human placental bi
41	265	28.0	128	W30050	Human placental bi
42	261	27.5	128	W30050	Human placental bi
43	259	27.3	128	W30050	Human placental bi
44	255	26.9	128	W30050	Human placental bi
45	254.5	26.8	124	W30050	Human placental bi

ALIGNMENTS

RESULT 1	W30041	Standard; Protein; 170 AA.
XX	W30041	Standard; Protein; 170 AA.
AC	W30041	Standard; Protein; 170 AA.
XX	W30041	Standard; Protein; 170 AA.
DT	20-APR-1998	(first entry)
XX	20-APR-1998	(first entry)
DE	Human placental, bikunin.	
KW	Human; placental bikunin; inhibition; trypsin; kallikrein;	
KW	plasma; factor xlla; treatment; prevention; oedema;	
KW	inflammation; infection; granulomatosis; multiple sclerosis;	
KW	ischaemia; peroperative blood loss; sepsis; shock; fibrosis;	
KW	blood coagulation disease; polytrauma; stroke; haemorrhage;	
XX	gastric cancer; cervical cancer; metastasis; blood loss.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PN	WO9733996-A2.	
XX	WO9733996-A2.	
PD	18-SEP-1997.	
XX	18-SEP-1997.	
PF	10-MAR-1997;	97WO-US03894.
XX	10-MAR-1997;	97WO-US03894.
PR	04-OCT-1996;	96US-0725251.
XX	04-OCT-1996;	96US-0725251.
PR	11-MAR-1996;	96US-0013106.
XX	11-MAR-1996;	96US-0013106.
PR	14-JUN-1996;	96US-0019793.
XX	14-JUN-1996;	96US-0019793.
PA	(FARB) BAYER CORP.	
XX	(FARB) BAYER CORP.	
PI	Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;	
XX	Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;	
DR	WPI; 1997-470876/43.	
XX	WPI; 1997-470876/43.	

PR New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss

XX Claim 1, Page 65; 110pp; English.

XX The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor X11a.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.

XX Sequence 170 AA;

Query Match 100.0%; Score 948; DB 18; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADDRESSHDFCLVSVYVGRCRASMPRMWYNTDGSQCLFVYGGCDGNSNNYLTKKECLKK 60

DB 1 addresshdfclvsvygrcrasmprrwvnyvdgscqlfvygdcgnsnnyltkkeclkk 60

QY 61 CATVTENATGDLATSRNADSSVPSAPRRQDSEHSDMFNEEYECTANAVGPCRASFP 120

DB 61 catvtenatgdlatsrnaadssvpsaprrqdsedhsdmfneyectanavgpcrafp 120

QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYSEBACMLRCFROENPPLPLGSK 170

DB 121 rwyfdvernsCNNFIYGGCRGNKNSYSEBACMLRCFROENPPLPLGSK 170

RESULT 2
W30053 standard; Protein: 179 AA.

W30053;

20-APR-1998 (first entry)

Human placental bikunin.

XX Human; placental bikunin; inhibition; trypsin; kallikrein;
XX plasmin; factor X11a; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.

XX Homo sapiens.

XX WO9733996-A2.

XX 18-SEP-1997.

XX 10-MAR-1997; 97WO-US03894.

XX 04-OCT-1996; 96US-0725251.

PR 11-MAR-1996; 96US-0013106.

PR 14-JUN-1996; 96US-0019793.

XX (FARB) BAYER CORP.

XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

XX WPI; 1997-470876/43.

XX New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss

XX Claim 1, Page 67; 110pp; English.

XX The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor X11a.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.

XX Sequence 179 AA;

Query Match 100.0%; Score 948; DB 18; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.3e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADDRESSHDFCLVSVYVGRCRASMPRMWYNTDGSQCLFVYGGCDGNSNNYLTKKECLKK 60

DB 1 addresshdfclvsvygrcrasmprrwvnyvdgscqlfvygdcgnsnnyltkkeclkk 60

QY 61 CATVTENATGDLATSRNADSSVPSAPRRQDSEHSDMFNEEYECTANAVGPCRASFP 120

DB 61 catvtenatgdlatsrnaadssvpsaprrqdsedhsdmfneyectanavgpcrafp 120

QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYSEBACMLRCFROENPPLPLGSK 170

DB 121 rwyfdvernsCNNFIYGGCRGNKNSYSEBACMLRCFROENPPLPLGSK 170

RESULT 3

W30043 standard; Protein: 197 AA.

W30043;

20-APR-1998 (first entry)

Human placental bikunin.

XX Human; placental bikunin; inhibition; trypsin; kallikrein;
XX plasmin; factor X11a; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.

XX Homo sapiens.

XX OS

PN W09733996-A2.
 XX 18-SEP-1997.
 XX 10-MAR-1997; 97WO-US03894.
 XX 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX (FARB) BAYER CORP.
 XX
 PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX WPI; 1997-470876/43.
 PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 XX Claim 1; Page 65; 110pp; English.
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 CC
 CC Sequence 197 AA;
 SQ
 Query Match 100.0%; Score 948; DB 18; Length 197;
 Best Local Similarity 100.0%; Pred. No. 1.4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 ADDRESSHDFCLVSKVYGRCSRAMPWWNYVTGSCQLFYTGCGDGSNNYLTKEECLK 60
 Db 19 addresshdfclvskvgrcrasmprrwvnyvtgscqlfytgscdgsnnyltkееclK 78
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRDSEHSSDMFNEYCYCANAVTGPCRASFP 120
 Db 79 catvtenatgdlatsrnaadssvpsaprrqdsedhsdmfneyeyctanaavtgpccrasfp 138
 QY 121 RWTFDVERNSCNFFITYGCGRGNKNSYRSEACMLRCFRQDNPPLPLGSK 170
 Db 139 rwyfdvernschnffiyggrgnknsyrseacmlrcfrqgenpplplgsk 188
 RESULT 4
 W30042
 ID W30042 standard; Protein; 213 AA.
 XX W30042;
 AC
 XX 20-APR-1998 (first entry)
 DT
 XX Human placental bikunin.
 DE
 XX Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW

KW Plasmin; factor XIIa; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX Homo sapiens.
 XX
 XX W09733996-A2.
 XX 18-SEP-1997.
 XX 10-MAR-1997; 97WO-US03894.
 XX 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX (FARB) BAYER CORP.
 XX
 PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX WPI; 1997-470876/43.
 PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 XX Claim 1; Page 65; 110pp; English.
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 CC
 CC Sequence 213 AA;
 SQ
 Query Match 100.0%; Score 948; DB 18; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.6e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADDRESSHDFCLVSKVYGRCSRAMPWWNYVTGSCQLFYTGCGDGSNNYLTKEECLK 60
 Db 1 addresshdfclvskvgrcrasmprrwvnyvtgscqlfytgscdgsnnyltkееclK 78
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRDSEHSSDMFNEYCYCANAVTGPCRASFP 120
 Db 61 catvtenatgdlatsrnaadssvpsaprrqdsedhsdmfneyeyctanaavtgpccrasfp 138
 QY 121 RWTFDVERNSCNFFITYGCGRGNKNSYRSEACMLRCFRQDNPPLPLGSK 170
 Db 121 rwyfdvernschnffiyggrgnknsyrseacmlrcfrqgenpplplgsk 170
 RESULT 5
 W30046
 ID W30046 standard; Protein; 225 AA.
 KW

XX AC W30046;
 XX DT 20-APR-1998 (first entry)
 XX DE Human placental bikunin.
 XX KW Human: placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor XIIa; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX OS Homo sapiens.
 XX PN W09733996-A2.
 XX PD 18-SEP-1997.
 XX 10-MAR-1997; 97WO-US03894.
 XX 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 PA (FARB) BAYER CORP.
 XX PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX WPI: 1997-470876/43.
 XX DR New human placental bikunin - used to inhibit kallikrein, trypsin
 XX PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 XX PF perioperative blood loss
 XX PS
 XX Claim 1; Page 66; 110pp; English.
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC apocitin, but is less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 CC
 CC Sequence 225 AA;
 SQ
 Query Match 100.0%; Score 948; DB 18; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.7e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ADDRESSIDFCLVSKVRCRASMPFRMYNTYDSCOLFVYGGCGNSNNYTKKECLK 60
 DB 1 addressidfclyskvrcrasmpfrmyntydgscqlfvyggcgnsnytkkeclkh 60
 OY 61 CATVFNATGDLATSRNADSSVPSAPRRDSESDSSDMFNTEYCTANAVTGPCRASFP 120
 DB 61 catvfnatgdlatsrnaadssvpsaprrdsehdhssdmfnueyctanavtgpccrasfp 120

OY 121 RMYEDVERNSCNNTYGGCRGNKNSRSEACMLRCFROENPPLPLGSK 170
 DB 121 rwyfdvernscnntfyggcrgnknksrseacmllrcfrqenppplp1gsk 170
 RESULT 6
 W30060
 ID W30060 standard; Protein; 235 AA.
 AC W30060;
 XX DT 20-APR-1998 (first entry)
 XX DE Human consensus bikunin.
 XX KW Human: consensus bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor XIIa; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX OS Homo sapiens.
 XX PN W09733996-A2.
 XX PD 18-SEP-1997.
 XX 10-MAR-1997; 97WO-US03894.
 XX 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 PA (FARB) BAYER CORP.
 XX PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX WPI: 1997-470876/43.
 XX DR N-PSDB; T90732.
 XX PT New human placental bikunin - used to inhibit kallikrein, trypsin
 XX PF etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 XX PS perioperative blood loss
 XX Disclosure; Fig 3; 110pp; English.
 CC The present sequence is a consensus human bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC apocitin, but is less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor

CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 CC
 XX
 SQ Sequence 235 AA;

Query Match 100.0%; Score 948; DB 18; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.8e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADDRESSHDFCLVSKVYGRASMPRWYNTDSCQLFYVGGCDGNSNNYLKKECLK 60
 Db 19 addresshdfclvskvgrcrasmprrwvntdsgcqlfyvgcdgnsnnylkkeclck 78
 QY 61 CATVTENATGDIATSRNAADSSVPSAPRRDSEHSSDMFYEEYCTANAVTGPCRASFP 120
 Db 79 catvtenatgdiatsrnaadssvpsaprrdsehssdmfyeeactanavtgpccrasfp 138
 121 RWFEDVERNSCNFFIYGCGRGNKNSYRSEBACMLRCFROENPPLPGSK 170
 139 rwyfdivernscnffiyggrgnknsyrseacmrlrcfrqenpplpgsk 188

RESULT 7
 W30045
 ID W30045 standard; Protein; 240 AA.
 AC W30045;

DT 20-APR-1998 (first entry)
 DE Human placental bikunin.

Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor Xlla; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.

OS Homo sapiens.
 XX
 PN WO9733996-A2.
 XX
 PD 18-SEP-1997.
 XX
 10-MAR-1997; 97WO-US03894.
 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX
 PA (FARB) BAYER CORP.

PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 DR WPI: 1997-470876/43.
 DR N-PSDB: T90734.

PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss

PS Claim 1; Page 66; 110pp; English.

CC The present sequence is human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor Xlla.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical

CC Cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 CC
 XX
 SQ Sequence 240 AA;

Query Match 100.0%; Score 948; DB 18; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.8e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADDRESSHDFCLVSKVYGRASMPRWYNTDSCQLFYVGGCDGNSNNYLKKECLK 60
 Db 28 addresshdfclvskvgrcrasmprrwvntdsgcqlfyvgcdgnsnnylkkeclck 67
 QY 61 CATVTENATGDIATSRNAADSSVPSAPRRDSEHSSDMFYEEYCTANAVTGPCRASFP 120
 Db 88 catvtenatgdiatsrnaadssvpsaprrdsehssdmfyeeactanavtgpccrasfp 147
 QY 121 RWFEDVERNSCNFFIYGCGRGNKNSYRSEBACMLRCFROENPPLPGSK 170
 Db 148 rwyfdivernscnffiyggrgnknsyrseacmrlrcfrqenpplpgsk 197

RESULT 8
 W30044
 ID W30044 standard; Protein; 248 AA.
 AC W30044;

DT 20-APR-1998 (first entry)

DE Human consensus bikunin.

Human; consensus bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor Xlla; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.

OS Homo sapiens.
 XX
 PN WO9733996-A2.
 XX
 PD 18-SEP-1997.
 XX
 10-MAR-1997; 97WO-US03894.
 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX
 PA (FARB) BAYER CORP.

PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 DR WPI: 1997-470876/43.
 DR N-PSDB: T90734.

PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss

PS Claim 1; Page 66; 110pp; English.

XX The present sequence is a consensus human bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC apocitin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.

Sequence 248 AA:

Query Match 100.0%; Score 948; DB 18; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-89; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 1 ADRERSIHDFCLVSKVYGRGRASMPRMWYNTDSCQLFYVGGDGNMNYLTKEECLK 60
DB 24 adrrsindhclvskvgrgrasmprrwvnyntdsgqlfyvggdgnsnmyltkeekl 83

QY 61 CATYENATGDLATSRNAADSSVPSAPRRDSEHSSDMFYECYCTANATGCRASFP 120
DB 84 catyenatgdlatsrnaadssvpsaprrdgsedhssdmfyecyctanaavtgcrafp 143

QY 121 RWFYDVERNSCNMFYVGGCRGNKNSYRSEACMLRCFRQENPPLPGSK 170
DB 144 rwyfdvernsnfmfyvgcrgnknysrseacmlrcfrqenpplpgsk 193

RESULT 9
W30040 ID W30040 standard; Protein; 252 AA.

AC W30040;

XX 20-APR-1998 (first entry)

Human placental bikunin.

XX Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.

OS Homo sapiens.

XX WO9733996-A2.

PN 18-SEP-1997.

XX 10-MAR-1997; 97WO-US03894.

XX 04-OCT-1996; 96US-0725251.

PR 11-MAR-1996; 96US-0013106.

PR 14-JUN-1996; 96US-0019793.

XX (FARB) BAYER CORP.

PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

DR WPI: 1997-470876/43.

DR N-PDB; T90731.

PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss

PS Claim 1; Page 65; 110pp; English.

XX The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC apocitin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.

Sequence 252 AA:

Query Match 100.0%; Score 948; DB 18; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.9e-89; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 1 ADRERSIHDFCLVSKVYGRGRASMPRMWYNTDSCQLFYVGGDGNMNYLTKEECLK 60
DB 28 adrrsindhclvskvgrgrasmprrwvnyntdsgqlfyvggdgnsnmyltkeekl 87

QY 61 CATYENATGDLATSRNAADSSVPSAPRRDSEHSSDMFYECYCTANATGCRASFP 120
DB 88 catyenatgdlatsrnaadssvpsaprrdgsedhssdmfyecyctanaavtgcrafp 147

QY 121 RWFYDVERNSCNMFYVGGCRGNKNSYRSEACMLRCFRQENPPLPGSK 170
DB 148 rwyfdvernsnfmfyvgcrgnknysrseacmlrcfrqenpplpgsk 197

RESULT 10
W13665 ID W13665 standard; Protein; 252 AA.

AC W13665;

XX 11-NOV-1997 (first entry)

XX Hepatocyte growth factor activator inhibitor HAI-II.

XX Hepatocyte growth factor activator inhibitor; HAI-II; HGF; human;

XX protease inhibitor.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..27

XX Protein /label= Sig_peptide

XX EP758682-A2.

XX 19-FEB-1997.
 PD 23-JUL-1996; 96EP-0111861.
 XX 24-JUL-1995; 95JP-0187134.
 PR (MITU) MITSUBISHI CHEM CORP.
 XX
 PI Kawauchi T, Kitamura N, Shimomura T;
 DR WPI: 1997-134770/13.
 DR N-PSDB; T61439.
 XX
 PT Novel protein HAI-II - inhibits protease activity of hepatocyte
 PT growth factor activator
 PS
 XX
 PS Claim 4; Page 18-19; 24pp; English.
 CC This sequence comprises a novel protein, designated HAI-II,
 CC that inhibits the protease activity of hepatocyte growth factor
 CC (HGF) activator. The sequence was deduced from a cDNA clone
 CC (T61439) obtained from cancer cell line MN45. Also claimed
 CC are isolated peptides (W13662-64) of HAI-II, the DNA encoding
 CC HAI-II, a vector carrying this DNA, and a host cell, pref. an
 CC animal cell, transformed with the vector. HAI-II can be used for
 CC regulating HGF activator activity (and thus HGF activity) in vitro
 CC and in vivo. It may also be used for investigating the function of
 CC HAI-II in vivo and the effect of HAI-II in hepatic disorders.
 XX
 SQ Sequence 252 AA;

Query Match 100.0%; Score 948; DB 19; Length 252;
 Best Local Similarity 100.0%; Pred. No. 1.9e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADDRESSHDFCLVSKVYGRASMPRMWYNTDSCQLFVYGGCDGNSNNYLTKEECLK 60
 DB 28 addresshdfclvskvgrasmprrwvnyvldgscqlfvyggcdgnsnnyltkeecik 87
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRDSEHSSDMFNEYECTANAVTGPCRASFP 120
 DB 88 catvtenatgdlatsrnaadssvpsaprrdgsedhssdmfneyectanavtgpccrasfp 147
 QY 121 RWFPEVERNSCNNFIYGGCRGNKNSYRSEACMLRCRQENPPLPGSK 170
 DB 148 rwyfdvernschnfiyggcrgnknsyrseacmlrcrfqgenpplpgsk 197

RESULT 11
 ID W70286
 XX W70286 standard; Protein; 252 AA.
 AC W70286;
 DT 06-NOV-1998 (first entry)
 XX
 DE Human tissue factor pathway inhibitor-3 (TFPI-3).
 XX
 KW Human tissue factor pathway inhibitor-3; TFPI-3; blood clot; sepsis;
 KW fibrin clot; coronary occlusion; acute myocardial infarction;
 KW prophylaxis; peripheral arterial embolism; inflammatory disease;
 KW transplant rejection; anticoagulant; blood transfusion;
 KW extracorporeal circulation; dialysis; haemophili; Kunitz type domain.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key
 FT Peptide 1..27
 FT Protein /note= "Signal peptide"
 FT 28..252
 FT /note= "TFPI-3"

XX WO9833920-A2.
 XX 06-AUG-1998.
 PD 27-JAN-1998; 98WO-US01468.
 XX 31-JAN-1997; 97US-0036703.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Gentz RL, Hsu T, Ni J, Rosen CA;
 DR WPI: 1998-437473/37.
 DR N-PSDB; V33063.
 XX
 PT Isolated tissue factor pathway inhibitor-3 - used to develop
 PT products for treating, e.g. pulmonary embolism, thrombosis, sepsis,
 PT inflammatory disease, transplant rejection or haemophilia
 XX
 PS Disclosure; Fig 1A-1B; 57pp; English.
 CC The present sequence represents a human tissue factor pathway
 CC inhibitor-3 (TFPI-3) which contains two Kunitz type domains. The
 CC invention also provides the TFPI-3 cDNA and screening methods for
 CC identifying agonists and antagonists of TFPI-3. As TFPI-3 inhibits
 CC protease activity, it is claimed to be useful for, e.g. inhibiting
 CC intravascular clotting and preventing the formation of fibrin clots
 CC both in vitro and in vivo, for treating coronary occlusion with acute
 CC myocardial infarction and in the prophylaxis and treatment of
 CC diseases and transplant rejection. The treatment of sepsis, inflammatory
 CC as an anticoagulant in blood transfusions, extracorporeal circulation,
 CC and dialysis procedures and in blood samples for laboratory purposes.
 CC The TFPI-3 antagonists are claimed to be useful for promoting
 CC coagulation, e.g. in the treatment of haemophilia.
 XX
 SQ Sequence 252 AA;

Query Match 100.0%; Score 948; DB 19; Length 252;
 Best Local Similarity 100.0%; Pred. No. 1.9e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADDRESSHDFCLVSKVYGRASMPRMWYNTDSCQLFVYGGCDGNSNNYLTKEECLK 60
 DB 28 addresshdfclvskvgrasmprrwvnyvldgscqlfvyggcdgnsnnyltkeecik 87
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRDSEHSSDMFNEYECTANAVTGPCRASFP 120
 DB 88 catvtenatgdlatsrnaadssvpsaprrdgsedhssdmfneyectanavtgpccrasfp 147
 QY 121 RWFPEVERNSCNNFIYGGCRGNKNSYRSEACMLRCRQENPPLPGSK 170
 DB 148 rwyfdvernschnfiyggcrgnknsyrseacmlrcrfqgenpplpgsk 197

RESULT 12
 ID W30051
 XX W30051 standard; Protein; 153 AA.
 AC W30051;
 DT 20-APR-1998 (first entry)
 XX
 DE Human placental bikunin.
 XX
 KW Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor Xlla; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.

XX Homo sapiens.
OS WO9733996-A2.
XX 18-SEP-1997.
XX 10-MAR-1997: 97WO-US03894.
XX 04-OCT-1996: 96US-0725251.
XX 11-MAR-1996: 96US-0013106.
XX 14-JUN-1996: 96US-0019793.
XX (FARB) BAYER CORP.
XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX WPI; 1997-470876/43.
XX New human placental bikunin - used to inhibit kallikrein, trypsin
XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX perioperative blood loss
XX Claim 1; Page 67; 110pp; English.
XX The present sequence is a human placental bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor X1a.
XX Bikunin can be used to treat or prevent brain and spinal cord
XX oedema, inflammation, infection or granulomatosis, multiple
XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX fibrosis, blood coagulation diseases, polytrauma, stroke,
XX cerebral or subarachnoid haemorrhage and gastric or cervical
XX cancer and prevent metastasis. It is particularly useful for
XX reducing blood loss during surgery, and can also be used to treat
XX other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX influenza and similar viral infections, acute pancreatitis and
XX gout, and prevent pre-term labour. It has similar properties to
XX aprotinin, but is less highly charged so should be less
XX immunogenic and less likely to damage the kidneys. Manipulation
XX of the bikunin sequence may allow the inhibitory profile to be
XX altered. It also reduces or eliminates the need for whole donor
XX blood or blood products during surgery, thereby reducing the risk
XX of infection and other adverse side effects, as well as reducing
XX the cost of surgery.
XX Sequence 153 AA:
SQ
Query Match 90.6%; Score 859; DB 18; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 IHDFCLVSKVGRGRASMPRMWYNTDGSQQLFVYGGCGNSNNYTKRECLKCAVTE 66
Db 1 ihdfclvskvgrcraemprrwvnytdgscqlfvyggcdgnsnnytkreclkkcatve 60
QY 67 NATGDLATSRNADSVPSAPRRODSEHSSDMFNEYECYCANAVTGPCRASFPWYDFV 126
Db 61 natgdlatsrnaadsvpsaprrdsehsdmsmfneyecytanavtgpccrasfpwydfv 120
QY 127 ERNSCNFIYGGCRGNKNSYRSEACMLRCFRQ 159
Db 121 ernscnfiyggcrgnknksyrseacmlrcfrq 153

RESULT 13
W30052
ID W30052 standard; Protein; 146 AA.
XX W30052;
AC W30052;
XX 20-APR-1998 (first entry)
DT
XX

DE Human placental bikunin.
XX Human; placental bikunin; inhibition; trypsin; kallikrein;
XX plasmin; factor X1a; treatment; prevention; oedema;
XX inflammation; infection; granulomatosis; multiple sclerosis;
XX ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
XX blood coagulation disease; polytrauma; stroke; haemorrhage;
XX gastric cancer; cervical cancer; metastasis; blood loss.
XX Homo sapiens.
XX WO9733996-A2.
XX 18-SEP-1997.
XX 10-MAR-1997: 97WO-US03894.
XX 04-OCT-1996: 96US-0725251.
XX 11-MAR-1996: 96US-0013106.
XX 14-JUN-1996: 96US-0019793.
XX (FARB) BAYER CORP.
XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX WPI; 1997-470876/43.
XX New human placental bikunin - used to inhibit kallikrein, trypsin
XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX perioperative blood loss
XX Claim 1; Page 67; 110pp; English.
XX The present sequence is a human placental bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor X1a.
XX Bikunin can be used to treat or prevent brain and spinal cord
XX oedema, inflammation, infection or granulomatosis, multiple
XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX fibrosis, blood coagulation diseases, polytrauma, stroke,
XX cerebral or subarachnoid haemorrhage and gastric or cervical
XX cancer and prevent metastasis. It is particularly useful for
XX reducing blood loss during surgery, and can also be used to treat
XX other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX influenza and similar viral infections, acute pancreatitis and
XX gout, and prevent pre-term labour. It has similar properties to
XX aprotinin, but is less highly charged so should be less
XX immunogenic and less likely to damage the kidneys. Manipulation
XX of the bikunin sequence may allow the inhibitory profile to be
XX altered. It also reduces or eliminates the need for whole donor
XX blood or blood products during surgery, thereby reducing the risk
XX of infection and other adverse side effects, as well as reducing
XX the cost of surgery.
XX Sequence 146 AA:
SQ
Query Match 86.4%; Score 819; DB 18; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.6e-76;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 CLVSKVGRGRASMPRMWYNTDGSQQLFVYGGCGNSNNYTKRECLKCAVTEATG 70
Db 1 clvskvgrcraemprrwvnytdgscqlfvyggcdgnsnnytkreclkkcatvtenatg 65
QY 71 DLATSRNADSVPSAPRRODSEHSSDMFNEYECYCANAVTGPCRASFPWYDFV 130
Db 61 dlatrnaadsvpsaprrdsehsdmsmfneyecytanavtgpccrasfpwydfv 120
QY 131 CNMFIYGGCRGNKNSYRSEACMLRC 156
Db 121 cnmfiyggcrgnknksyrseacmlrc 146

CC the cost of surgery.

Sequence	92 AA;
SQ	

Query Match	52.8%	Score 501;	DB 18;	Length 92;
Best Local Similarity	100.0%	Pred. No. 3.3e-44;		
Matches	92;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 ADERSIHDECLVSKVVGRCRASHPRMWNYNITDGSCLQVIVGCCGNSNNILENDBCCN
|||||
Db 1 adersihdfclvskvvgrcrasmprmwynvtdgscqlfvyygcgdnsmnltkeecik 60

61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
|||||

Db 61 catvtentatgdlatsrnaadssvpaprrqds 92

Search completed: January 31, 2001, 15:03:02
 Job time: 23 sec

Search completed: January 31, 2001, 15:03:02
 Job time: 23 sec

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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:03:28 ; Search time 12.37 Seconds
(without alignments)
246.782 Million cell updates/sec

Title: US-09-441-654A-1
948

Sequence: 1 ADRESDHDFCLVSKVVGRC.....ACMLRCFRQGNPLPLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	948	100.0	252	1	US-08-685-660A-7
2	948	100.0	252	1	US-08-974-196-7
3	247.5	26.1	122	2	US-08-422-333-12
4	247.5	26.1	122	5	5187153-20
5	247.5	26.1	122	5	5220013-23
6	244.5	25.8	143	2	US-08-422-333-10
7	244.5	25.8	143	5	5223482-20
8	244.5	25.8	144	5	5187153-18
9	244.5	25.8	147	1	US-08-358-160-72
10	243.5	25.7	127	5	5466783-24
11	241.5	25.5	123	5	5466783-21
12	233.5	24.6	122	5	5223482-22
13	233.5	24.6	276	1	US-07-828-920A-1
14	233.5	24.6	276	1	US-08-437-841-9
15	233.5	24.6	276	1	US-08-286-521-9
16	233.5	24.6	276	1	US-08-436-175-9
17	233.5	24.6	276	2	US-08-796-850-1
18	233.5	24.6	276	2	US-08-437-841-19
19	233.5	24.6	276	4	PCT-US95-09377-3
20	233.5	24.6	276	4	PCT-US95-09464-9
21	233.5	24.6	277	1	US-07-844-297-1
22	233.5	24.6	304	1	US-08-026-145-2
23	233.5	24.6	304	1	US-08-446-646-6
24	233.5	24.6	304	1	US-08-676-125A-18
25	233.5	24.6	304	2	US-09-136-012A-18
26	233.5	24.6	304	2	US-08-676-124-1
27	233.5	24.6	304	3	US-08-208-264A-25
28	233.5	24.6	304	3	US-09-414-878-1

29	233.5	24.6	304	3	US-09-240-136-1	Sequence 1, Appl
30	233.5	24.6	304	5	5466783-2	Patent No. 5466783
31	233.5	24.6	352	3	US-08-854-764-2	Sequence 2, Appl
32	233.5	24.6	352	4	PCT-US95-09377-2	Patent No. 5466783
33	233.5	24.5	123	5	5466783-22	Patent No. 5466783
34	232	24.5	161	1	US-08-437-841-19	Sequence 19, Appl
35	232	24.5	161	1	US-08-286-521-19	Sequence 19, Appl
36	232	24.5	161	1	US-08-436-175-19	Sequence 19, Appl
37	232	24.5	161	4	PCT-US95-09464-19	Sequence 19, Appl
38	230	24.3	122	5	5466783-23	Patent No. 5466783
39	228	24.1	183	1	US-07-828-920A-5	Sequence 1, Appl
40	226	23.8	189	1	US-07-828-920A-7	Sequence 1, Appl
41	219	23.1	213	5	5466783-25	Patent No. 5466783
42	214.5	22.6	213	2	US-08-796-850-2	Sequence 2, Appl
43	214.5	22.6	235	1	US-08-147-710-2	Sequence 2, Appl
44	214.5	22.6	235	1	US-08-458-090-2	Sequence 2, Appl
45	214.5	22.6	235	2	US-08-457-887-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-685-660A-7
; Sequence 7, Application US/08685660A
; Patent No. 5731412
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SOGHROE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,660A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hel 7-187134
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-42295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-660A-7

Query Match 100.0%; Score 948; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-92;
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

1 ADRESDHDFCLVSKVVGRCASRMWYNTDSCOLFVGGCGGNSNNTLREBCLAK 60
|||||

Wed Jan 31 15:19:33 2001

us-09-441-654a-1.ra1

Page 2

Db 28 ADERSIHDECLVSKVYGRCRASMPRWYNTDSCQLFYGGCGDGSNNYLKKECLK 87
QY 61 CATVTENATGDLATSRNADSVSPAPRRDSEHSSDMFNIEEYCTAANAATGPCRASFP 120
Db 88 CATVTENATGDLATSRNADSVSPAPRRDSEHSSDMFNIEEYCTAANAATGPCRASFP 147
QY 121 RWFYDVERNSCNNFYGGCGRGNKNSYRSEACMLRCFROENPPLPLGSK 170
Db 148 RWFYDVERNSCNNFYGGCGRGNKNSYRSEACMLRCFROENPPLPLGSK 197

RESULT 2
US-08-974-196-7
; Sequence 7, Application US/08974196
; Patent No. 5854396
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KAWAGUCHI, Toshiya
APPLICANT: KITAMURA, Naomi
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR "SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,196
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,660
FILING DATE: 24-JUL-1996
APPLICATION NUMBER: JPA Hel 7-187134
FILING DATE: 24-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: Q-42295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-196-7

Query Match 100.0%; Score 948; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-92; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 1 ADERSIHDECLVSKVYGRCRASMPRWYNTDSCQLFYGGCGDGSNNYLKKECLK 60
Db 28 ADERSIHDECLVSKVYGRCRASMPRWYNTDSCQLFYGGCGDGSNNYLKKECLK 87
QY 61 CATVTENATGDLATSRNADSVSPAPRRDSEHSSDMFNIEEYCTAANAATGPCRASFP 120
Db 88 CATVTENATGDLATSRNADSVSPAPRRDSEHSSDMFNIEEYCTAANAATGPCRASFP 147
QY 121 RWFYDVERNSCNNFYGGCGRGNKNSYRSEACMLRCFROENPPLPLGSK 170
Db 148 RWFYDVERNSCNNFYGGCGRGNKNSYRSEACMLRCFROENPPLPLGSK 197

RESULT 3
US-08-422-333-12
; Sequence 12, Application US/08422333
; Patent No. 5912410
GENERAL INFORMATION:
APPLICANT: CORDELL, Barbara L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE ANTIOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scios, Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-12

Query Match 26.1%; Score 247.5; DB 2; Length 122;
Best Local Similarity 32.4%; Pred. No. 6e-19;
Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

QY 9 DECLVSKVYGRCRASMPRWYNTDSCQLFYGGCGDGSNNYLKKECLKCATYTENA 68
Db 3 DSCQLDYSQGPCLGLFRFYNGTSMACETFLYGGCGMGLNPLSOKECLOTCTRY---- 58
QY 69 TGDPLATSRNADSVSPAPRRDSEHSSDMFNIEEYCTAANAATGPCRASFPWFYDVER 128
Db 59 -----EACNLPLIYOGCRAFIOLMADAVK 83
QY 129 NSCNNFYGGCGRGNKNSYRSEACMLRC 156
Db 84 GKCVRFSGCGCKGNGKNKFSQKCKEYIC 111

RESULT 4
5187153-20
; Patent No. 5187153
APPLICANT: CORDELL, BARBARA, SCHILLING, JAMES W., KATUNUMA, NOBUHIKO
TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; ANTIOID POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/502,273
FILING DATE: 29-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 361,912
FILING DATE: 06-JUN-1989

RESULT 6
 US-08-422-333-10
 Sequence 10, Application US/08422333
 Patent No. 5912410
 GENERAL INFORMATION:
 APPLICANT: CORDELL, Barbara L.
 TITLE OF INVENTION: TRANSCENT NON-HUMAN MAMMAL DISPLAYING
 TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scios, Inc.
 STREET: 2450 Bayshore Parkway
 CITY: Mountain View
 STATE: CA
 COUNTRY: USA
 ZIP: 94043
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/422,333
 FILING DATE: 13-APR-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Shearer, Peter R.
 REGISTRATION NUMBER: 28,117
 REFERENCE/DOCKET NUMBER: 21900-28048.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 966-1550
 TELEFAX: (415) 968-2438
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 143 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-422-333-10

FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 20
LENGTH: 143
5223482-20

Query Match 25.8%; Score 244.5; DB 5; Length 143;
Best Local Similarity 31.8%; Pred. No. 1.5e-18;
Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;

QY 9 DCLVSKVYGRCRASMPRMWYNTDSCQLFYVGGCDGNSNNYLTKECKLKCATVTENA 68
DB 24 DSCQLGYSAGPCMGMTSRFYNGTSMACEFQYGGCGMGNNNVTREKCLQTCRTVA-- 81
69 TGDLSRNAADSSVPSAPRRQDSEHSSDMFYEEYCTANAVTGPCRASFPWMYDVER 128
DB 82 -----CNLPYIRGPCRAFIOLMADAVK 104

QY 129 NSCNNFIYGGCRGNKNSYSEACMLRC 156
DB 105 GKCVLFPGYGGCGGNKNTYSEKREYEC 132

RESULT 8
5187153-18
PATENT NO. 5187153
APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
AMLOID POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/502,273
FILING DATE: 29-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 361,912
FILING DATE: 06-JUN-1986
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 18
LENGTH: 144
5187153-18

Query Match 25.8%; Score 244.5; DB 5; Length 144;
Best Local Similarity 31.8%; Pred. No. 1.5e-18;
Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;

QY 9 DCLVSKVYGRCRASMPRMWYNTDSCQLFYVGGCDGNSNNYLTKECKLKCATVTENA 68
DB 24 DSCQLGYSAGPCMGMTSRFYNGTSMACEFQYGGCGMGNNNVTREKCLQTCRTVA-- 81
69 TGDLSRNAADSSVPSAPRRQDSEHSSDMFYEEYCTANAVTGPCRASFPWMYDVER 128
DB 82 -----CNLPYIRGPCRAFIOLMADAVK 104

QY 129 NSCNNFIYGGCRGNKNSYSEACMLRC 156
DB 105 GKCVLFPGYGGCGGNKNTYSEKREYEC 132

RESULT 9
US-08-358-160-72
Sequence 72; Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iyer P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SHD ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-72

Query Match 25.8%; Score 244.5; DB 1; Length 147;
Best Local Similarity 32.4%; Pred. No. 1.6e-18;
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;

QY 9 DCLVSKVYGRCRASMPRMWYNTDSCQLFYVGGCDGNSNNYLTKECKLKCATVTENA 68
DB 24 DSCQLGYSAGPCMGMTSRFYNGTSMACEFQYGGCGMGNNNVTREKCLQTCRTVA-- 81
69 TGDLSRNAADSSVPSAPRRQDSEHSSDMFYEEYCTANAVTGPCRASFPWMYDVER 128


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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,920A
; FILING DATE: 19920127
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 4080/89
; FILING DATE: 18-AUG-1989
; APPLICATION NUMBER: WO PCT/DK90/00212
; FILING DATE: 17/AUG/1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Zelson, Steve T.
; REGISTRATION NUMBER: 30335
; REFERENCE/DOCKET NUMBER: 3287.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..276
;
US-07-828-920A-1

Query Match 24.6%; Score 233.5; DB 1; Length 276;
Best Local Similarity 33.6%; Pred. No. 5.1e-17;
Matches 51; Conservative 26; Mismatches 64; Indels 11; Gaps 3;

Qy 9 DFCIVSKVGRCRASPRWYVNTDGSQCLFYGGCDGNSNNYLTKECLKKCATVTENA 68
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 95 DFCLEEDPGICRGYITRYFYNNQTKQCFKYGCGCLGNMNNFETLECKNIC---EDGP 151
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 69 TG----DLATSRNAADSVPSAPRRQDSDHSDMFNFEYECTANAVTGPCRASFPWWYF 124
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 152 NGFQVDNYGTQLNAVNSLTP---QSTKVPSLFEFHGPSWCLTPADRGCLCRANENRFY 207
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 DVERNSCNFIYGGCGGNKNSYRSEACMLRC 156
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
208 NSVIGKCRPFYSGCGGNENFTSKQECRLAC 239
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-08-437-841-9
; Sequence 9, Application US/08437841
; Patent No. 5563123
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abia
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,521
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
```

```
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,521
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-437-841-9

Query Match 24.6%; Score 233.5; DB 1; Length 276;
Best Local Similarity 33.6%; Pred. No. 5.1e-17;
Matches 51; Conservative 26; Mismatches 64; Indels 11; Gaps 3;

Qy 9 DFCIVSKVGRCRASPRWYVNTDGSQCLFYGGCDGNSNNYLTKECLKKCATVTENA 68
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 95 DFCLEEDPGICRGYITRYFYNNQTKQCFKYGCGCLGNMNNFETLECKNIC---EDGP 151
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 69 TG----DLATSRNAADSVPSAPRRQDSDHSDMFNFEYECTANAVTGPCRASFPWWYF 124
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 152 NGFQVDNYGTQLNAVNSLTP---QSTKVPSLFEFHGPSWCLTPADRGCLCRANENRFY 207
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 DVERNSCNFIYGGCGGNKNSYRSEACMLRC 156
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
208 NSVIGKCRPFYSGCGGNENFTSKQECRLAC 239
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-08-286-521-9
; Sequence 9, Application US/08286521
; Patent No. 5589359
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abia
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,521
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
```

TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-286-321-9

Query Match 24.6%; Score 233.5; DB 1; Length 276;
Best Local Similarity 33.6%; Pred. No. 5.1e-17;
Matches 51; Conservative 26; Mismatches 64; Indels 11; Gaps 3;
QY 9 DFCLYSKVVGRGRASMPRWYNNVTDGSCQLFYGGCDGNSNNYLTKEECKLKCATVTENA 68
| | | : : | | | : | : | | | : | | | : | | | :
Db 95 DFCFLEEDPGICRGYITRYFYNNQTKQCFERKYGCGCLGNNNNFETLECKNIC---EDGP 151
69 TG---DLATSRNAADSSVPSAPRRQDSEHDHSSDMFNVEEYCTANAVTGPCRASFPRWYF 124
| : | | | : | : | : | : | : | : | : | : | : | : | :
Db 152 NGFQVDNYGTQLNAVNNSLTP----QSTKVPSLFEFHGPSWCLTPADRGLCRANENRFY 207
QY 125 DVERNSCNNFIYGGCGKNSYRSEACMLRC 156
| | | | | | | | | | | : | : | : | : | : | : | : | :
Db 208 NSVIGKCRPFKYGGCGGNNENFTSKQECULRAC 239

Search completed: January 31, 2001, 15:05:21
Job time: 113 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:05:08 ; Search time 15.54 Seconds
(without alignments)
742.800 Million cell updates/sec

Title: US-09-441-654A-1

Perfect score: 170

Sequence: 1 ADERSIHDFCLVSKVVGRC.....ACMLRCFRQENPPLGLGSK 170

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 195891 seqs, 67900655 residues

Id size: 0

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: PIR66:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	7.6	252	2 JG0185	hepatocyte growth
2	11	6.5	302	1 TIRTK	tissue factor path
3	9	5.3	58	1 TIRABK	isoactivator K (BP
4	9	5.3	65	1 TIVIVC	venom basic protei
5	8	4.7	922	2 T23573	hypothetical prote
6	8	4.7	973	2 S54534	coatomer complex b
7	8	4.7	1599	2 T16210	hypothetical prote
8	8	4.7	2844	2 S28291	hypothetical prote
9	7	4.1	57	1 TIFHBP	proteinase inhibit
10	7	4.1	61	1 TIRCBP	proteinase inhibit
11	7	4.1	62	1 S19327	venom basic protei
12	7	4.1	120	1 J01280	lipid transfer pro
13	7	4.1	125	1 TIRHBI	alpha-1-microglobu
14	7	4.1	183	2 T28711	hypothetical prote
15	7	4.1	210	2 S66484	insulin-like growt
16	7	4.1	253	2 S49183	hypothetical prote
17	7	4.1	438	2 T12494	hypothetical prote
18	7	4.1	500	2 F71978	hypothetical prote
19	7	4.1	507	2 H82378	probable long-chain
20	7	4.1	988	2 I50611	protein-tyrosine k
21	7	4.1	1663	1 C3HU	complement C3 prec
22	7	4.1	2167	2 T34395	hypothetical prote
23	7	4.1	2172	2 T20145	hypothetical prote
24	7	4.1	4660	2 T42737	gp330 protein prec
25	6	3.5	55	2 S30332	proteinase inhibit
26	6	3.5	56	2 JN0380	trypsin inhibitor
27	6	3.5	57	1 TIRIV2	venom basic protei
28	6	3.5	57	1 TIRIVC	venom basic protei
29	6	3.5	57	2 S13846	venom animal Kunit

ALIGNMENTS

RESULT 1

JG0185

hepatocyte growth factor activator inhibitor type 2 - mouse

C:Species: Mus musculus (House mouse)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C:Accession: JG0185

R:Itoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Koono, M.

Biochem. Biophys. Res. Commun. 255, 740-748, 1999

A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first

A:Reference number: JG0185; MUID:99160423

A:Accession: JG0185

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-252 <IIO>

A:Cross-references: GB:AF099016

C:Superfamily: animal Kunitz-type proteinase inhibitor homology

F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 7.6% Score 13; DB 2; Length 252;

Best Local Similarity 100.0%; Pred. No. 5.3e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 FIYGGCRGNKNSY 146

Db 161 FIYGGCRGNKNSY 173

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F:222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
 F:288-291/Region: heparin binding #status predicted
 F:53-103,62-86,78-99,124-174,133-157,149-170,222-272,231-255,247-268/Disulfide bonds: #s
 F:63/inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
 F:134/inhibitory site: Arg (coagulation factor X) #status predicted
 F:144,251,261/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:232/inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 6.5%; Score 11; DB 1; Length 302;

Best Local Similarity 100.0%; Pred. No. 0.00084; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0;

QY 134 FIYGGCRGNK 144

Db 81 FIYGGCRGNK 91

RESULT 3

TIHABK

A:Title: Helix pomatia (Roman snail)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994

C:Accession: A91232; A01225

R:Tschesche, H.; Dietl, T.

Eur J. Biochem. 58:439-451, 1975

A:Title: The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequen

A:Reference number: A91232; MUID:76043680

A:Accession: A91232

A:Molecule type: protein

A:Residues: 1-58 <TSC>

R:Dietl, T.; Tschesche, H.

Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976

A:Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergschnecken

A:Reference number: A91666; MUID:76141310

A:Contents: annotation; disulfide bonds

C:Comment: This is one of several isoinhibitors of broad specificity that are secreted i

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 5.3%; Score 9; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 0.027; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

134 FIYGGCRGN 142

35 FIYGGCRGN 43

RESULT 4

TIHABK

venom basic proteinase inhibitor III - sand viper

N:Alternate names: venom chymotrypsin inhibitor

C:Species: Vipera ammodytes (sand viper)

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Aug-1996

C:Accession: A01223

R:Bitonja, A.; Meloun, B.; Gubensek, F.

Biochim. Biophys. Acta 746, 138-145, 1983

A:Title: The primary structure of Vipera ammodytes venom chymotrypsin inhibitor.

A:Reference number: A01223

A:Accession: A01223

A:Molecule type: protein

A:Residues: 1-65 <RT>

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Disulfide bonds: #status predicted

F:17/Inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 5.3%; Score 9; DB 1; Length 65;

Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

QY 134 FIYGGCRGN 142

Db 35 FIYGGCRGN 43

RESULT 5

T23573

A:Title: Hypothetical protein:K10D3.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T23573

R:McMurray, A.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19762

A:Accession: T23573

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-922 <NII>

A:Cross-references: EMBL:275545; PIDN:CAA99886.1; GSPDB:GNO0019; CESP:K10D3.4

A:Experimental source: clone K10D3

C:Genetics:

A:Gene: CESP:K10D3.4

A:Map position: 1

A:Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 4.7%; Score 8; DB 2; Length 922;

Best Local Similarity 100.0%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0;

QY 43 GCDGNSNN 50

Db 552 GCDGNSNN 559

RESULT 6

S54534

N:Alternate names: protein YB8419.05c; protein YDR238C

C:Species: Saccharomyces cerevisiae

C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-Sep-1999

C:Accession: S54534; A55123; C55123; S50260

R:Oliver, K.; Harris, D.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54530

A:Accession: S54534

A:Molecule type: DNA

A:Residues: 1-973 <OLI>

A:Cross-references: EMBL:249701; NID:9817819; PIDN:CAA99724.1; PID:9817824; MIPS:1000

A:Experimental source: strain AB972

R:Duden, R.; Hosobuchi, M.; Hamamoto, S.; Winey, M.; Byers, B.; Schekman, R.

J. Biol. Chem. 269, 24486-24495, 1994

A:Title: Yeast beta'- and beta''-coat proteins (COP). Two coatmer subunits essential

A:Reference number: A55123; MUID:95014199

A:Accession: A55123

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-411, E', 413-973 <DUD>

A:Cross-references: GB:U11236; NID:9595412; PIDN:AAA61710.1; PID:9595413

A:Accession: C55123

A:Molecule type: protein

A:Residues: 353-362; 496-514; 645-655; 934-942 <DUD>

C:Genetics:

A:Gene: SGD:SEC26

A:Cross-references: SGD:S0002646; MIPS:YDR238C

A:Map position: 4R

C:Superfamily: coatmer complex beta chain

C:Keywords: blocked amino end; transmembrane protein

F:391-407/Domain: transmembrane #status predicted <TM1>
F:409-425/Domain: transmembrane #status predicted <TM2>
F:587-603/Domain: transmembrane #status predicted <TM3>

Query Match 4.7%; Score 8; DB 2; Length 973;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DLATSRNA 78
|||||
DB 347 DLATSRNA 354

RESULT 7
Ti6210
hypothetical protein F30H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Accession: T16210
Pauley, A.; Stelliyes, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F30H5.
A:Reference number: Z18478
A:Accession: T16210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1599 <PAU>
A:Cross-references: EMBL:U29096; NID:g861390; PID:g861393; PIDN:AAA68408.1; CESP:F30H5.3
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F30H5.3
A:Introns: 12/1; 59/2; 85/3; 124/3; 217/2; 534/3; 560/1; 1549/1

Query Match 4.7%; Score 8; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCDGNSNN 50
|||||
DB 704 GCDGNSNN 711

RESULT 8
S28291
Hypothetical protein ZC84.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
Accession: S28291
R:Thomas, K.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28285
A:Accession: S28291
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2844 <THO>
A:Cross-references: EMBL:Z19157
C:Genetics:
A:Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12493/1; 2555/1; 2720/1; 2739/3; 2819/1

C:Superfamily: animal Kunitz-type proteinase inhibitor homology
F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>
F:546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>
F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>
F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>
F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>
F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>
F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>
F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI10>

Query Match 4.7%; Score 8; DB 2; Length 2844;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCDGNSNN 50
|||||
DB 580 GCDGNSNN 587

RESULT 9
TIFHBP
proteinase inhibitor - flesh fly (Sarcophaga bullata)
C:Species: Sarcophaga bullata
C:Date: 07-Feb-1992 #sequence_revision 22-Jul-1994 #text_change 07-May-1993
C:Accession: A37294
R:Papayannopoulos, I.A.; Biemann, K.
Protein Sci. 1, 278-288, 1992
A:Title: Amino acid sequence of a protease inhibitor isolated from Sarcophaga
A:Reference number: A37294; MUID:93284121
A:Accession: A37294
A:Molecule type: protein
A:Residues: 1-57 <PAP>
A:Experimental source: hemolymph
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase
C:Keywords: serine proteinase inhibitor
F:6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:6-56,15-39,31-52/Disulfide bonds: #status predicted
F:16/Inhibitory site: Arg (chymotrypsin) #status predicted

Query Match 4.1%; Score 7; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 YGCGRGN 142
|||||
DB 36 YGCGRGN 42

RESULT 10
TIHCBP
proteinase inhibitor (BPI-type) - horseshoe crab (Tachyplesus tridentatus)
C:Species: Tachyplesus tridentatus
C:Date: 08-Mar-1989 #sequence_revision 22-Jul-1994 #text_change 24-Feb-1995
C:Accession: A26923
R:Nakamura, T.; Hirai, T.; Tokunaga, F.; Kawabata, S.; Iwanaga, S.
J. Biochem. 101, 1297-1306, 1987
A:Title: Purification and amino acid sequence of Kunitz-type protease inhibitor found
A:Reference number: A26923; MUID:88007472
A:Accession: A26923
A:Molecule type: protein
A:Residues: 1-61 <NAK>
A:Experimental source: hemocytes
C:Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: serine proteinase inhibitor
F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:8-58,17-41,33-54/Disulfide bonds: #status predicted
F:18/Inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, kallikrein)

Query Match 4.1%; Score 7; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 VTGPCRA 117
|||||
DB 13 VTGPCRA 19

RESULT 11
S19327

venom basic proteinase inhibitor - leaf-nosed viper
 N:Alternate names: trypsin inhibitor (Kunitz-type)
 C:Species: Eristocophis machahoni (leaf-nosed viper)
 C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 A:Accession: S19327
 R:Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.
 FEBS Lett. 294, 141-143, 1991
 A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
 A:Reference number: S19327; MUID:92077130
 A:Accession: S19327
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-62 <SID>
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C:Keywords: serine proteinase inhibitor; venom
 F:2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 Query Match 4.1%; Score 7; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 133 NFIYGGC 139
 Db 29 NFIYGGC 35
 RESULT 12
 JQ1280
 lipid transfer protein EP2 precursor - carrot
 N:Alternate names: extracellular protein 2
 C:Species: Daucus carota (carrot)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: JQ1280
 R:Sterk, P.; Boelj, H.; Schellekens, G.A.; Van Kammen, A.; De Vries, S.C.
 Plant Cell 3, 907-921, 1991
 A:Title: Cell-specific expression of the carrot EP2 lipid transfer protein gene.
 A:Reference number: JQ1280; MUID:92361243
 A:Accession: JQ1280
 A:Molecule type: mRNA
 A:Residues: 1-120 <ST>
 A:Cross-references: GB:M64746; NID:g167553; PIDN:AAB96834.1; PID:g167554
 C:Comment: This protein locates in cell walls.
 C:Comment: The gene encoding for this protein is expressed in the embryogenic cell cultu
 C:Superfamily: phospholipid transfer protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:27-120/Product: lipid transfer protein EP2 #status predicted <LIP>
 Query Match 4.1%; Score 7; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 107 TANAVTG 113
 Db 83 TANAVTG 89
 RESULT 13
 TIH0BI
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
 N:Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
 C:Species: Equus caballus (domestic horse)
 C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 05-May-2000
 A:Accession: A01210; A45653
 R:Hochstrasser, K.; Wächter, E.; Albrecht, G.J.; Reisinger, P.
 Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
 A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
 A:Reference number: A01210
 A:Accession: A01210
 A:Molecule type: protein
 A:Residues: 3-125 <HOC>
 R:Veeraragavan, K.; Singh, K.; Wächter, E.; Hochstrasser, K.

Biochem. Int. 26, 405-413, 1992
 A:Title: Characterization of a trypsin inhibitor from equine urine.
 A:Reference number: A45653; MUID:92328813
 A:Accession: A45653

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12, 'E', 14-33 <VEE>
 A:Cross-references: PIDN:AAB22430.1; PID:g250858
 A:Experimental source: urine
 A:Note: sequence extracted from NCBI backbone (NCBIP:107966)
 C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
 C:Comment: first domain interacts weakly with PMN-granulocytic elastase and not at all with panc
 C:Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
 C:elastase; those with leucine interact strongly.
 C:Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocal
 C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
 F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
 F:17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
 F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:73/Inhibitory site: Arg (trypsin) #status predicted

Query Match 4.1%; Score 7; DB 1; Length 125;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 YGGGRGN 142

Db 93 YGGGRGN 99

RESULT 14

T28711

hypothetical protein T21D12.12 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T28711

R:Woessner, J.

submitted to the EMBL Data Library, August 1997

A:Description: The sequence of C. elegans cosmid T21D12.

A:Reference number: Z20314

A:Accession: T28711

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-183 <WOE>

A:Cross-references: EMBL:AF016687; PIDN:AAC48097.1; GSPDB:GN00022; CESP:T21D12.12

A:Experimental source: strain Bristol N2; clone T21D12

C:Genetics:

A:Gene: CESP:T21D12.12

A:Map position: 4

A:Introns: 57/3; 88/1; 126/1; 147/2

Query Match 4.1%; Score 7; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCDGNSN 49

Db 58 GCDGNSN 64

RESULT 15

S66484

insulin-like growth factor II precursor - spiny dogfish

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C:Accession: S66484; S58053

R:Duguay, S.J.; Chan, S.J.; Mommsen, T.P.; Steiner, D.F.

FEBS Lett. 371, 69-72, 1995

A:Title: Divergence of insulin-like growth factors I and II in the elasmobranch, S.

A:Reference number: S66484; MUID:95394151
A:Accession: S66484
A:Molecule type: mRNA
A:Residues: 1-210 <DUG>
A:Cross-references: EMBL:Z50082; NID:g902732; PIDN:CAA90413.1; PID:g902733
A:Experimental source: liver
C:Superfamily: insulin
C:Keywords: growth factor
F:1-49/Domain: signal sequence #status predicted <SIG>
F:50-210/Product: insulin-like growth factor II #status predicted <MAT>
F:50-82/Domain: insulin chain B-like #status predicted <DOB>
F:83-90/Domain: insulin connecting peptide C-like #status predicted <CPE>
F:91-111/Domain: insulin chain A-like #status predicted <DOA>
F:112-117/Domain: Peptide D #status predicted <DOD>
F:118-210/Domain: carboxyl-terminal propeptide (E peptide) #status predicted <CHE>
F:58-97,70-110,96-101/Disulfide bonds: #status predicted

Query Match 4.1%; Score 7; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VSKVGR 19

|||||

Db 78 VSKVGR 84

Search completed: January 31, 2001, 15:07:08
Job time: 120 sec

Result No.	Score	Query %			ID	Description
		Match	Length	DB		
1	11	6.5	302	1	TFPI_RAT	Q02445 rattus norv
2	9	5.3	58	1	ISIK_HEIPO	P00994 helix pomat
3	9	5.3	65	1	IVB3_VIPRAA	P00992 vipera ammo
4	8	4.7	973	1	COPB_YEAST	P41810 saccharomyc
5	8	4.7	1416	1	YN81_CAEEL	Q03610 caenorhabdi
6	7	4.1	57	1	SBPI_SARBU	P26228 sarcophaga
7	7	4.1	61	1	IBPI_TACTR	P16044 tachypleus
8	7	4.1	62	1	IVBT_ERIMA	P24541 eristocophi
9	7	4.1	120	1	NLTP_DAUCA	P27631 gauscus caro
10	11	7	4.1	123	IATR_HORSE	P04365 equus cabal
11	7	4.1	521	1	TRPE_BUCAL	Q44695 buchnera ap
12	7	4.1	1663	1	CO3_HUMAN	P01024 homo sapien
13	7	4.1	4660	1	LRP2_RAT	P98158 rattus norv
14	6	3.5	52	1	ISP2_GALME	P81906 galleria me
15	6	3.5	55	1	ISH1_STOHE	P31713 stoichactis
16	6	3.5	55	1	ISH2_STOHE	P81129 stoichactis
17	6	3.5	56	1	ITR4_RADMA	P16344 radianthus
18	6	3.5	57	1	IVB2_HEMHA	P00985 hemachatus
19	6	3.5	57	1	IVB2_NAUNI	P00986 najia nivea
20	6	3.5	57	1	IVBT_NAJIN	P20229 najia najia (
21	6	3.5	60	1	IBPS_BOVIN	P00975 bos taurus
22	6	3.5	61	1	ITRS_RAT	P19603 rattus norv
23	6	3.5	61	1	IVB1_VIPAA	P00991 vipera ammo
24	6	3.5	62	1	IP52_ANFSU	P10280 anemonia su
25	6	3.5	62	1	ISCI_BOMMO	P10831 bombyx mori
26	6	3.5	62	1	ISCS2_BOMMO	P10832 bombyx mori
27	6	3.5	63	1	ICS3_BOMMO	P07481 bombyx mori
28	6	3.5	63	1	IMAP_DROFU	P11424 drosofila
29	6	3.5	69	1	CRPT_BOOMI	P81162 boophilus m
30	6	3.5	76	1	A4_MACMU	P29216 macaca mula
31	6	3.5	76	1	Y8K9_VACCV	P07608 vaccinia vi
32	6	3.5	87	1	A4_MACFA	P53601 macaca fasc
33	6	3.5	94	1	S110_RAT	P05943 rattus norv

Wed Jan 31 15:14:33 2001

us-09-441-654a-1.oli.rsp

FT DOMAIN 222 272
 FT DISULFID 53 103
 FT DISULFID 62 86
 FT DISULFID 78 99
 FT DISULFID 78 99
 FT ACT_SITE 63 64
 FT DISULFID 124 174
 FT DISULFID 133 157
 FT DISULFID 149 170
 FT ACT_SITE 134 135
 FT DISULFID 222 272
 FT DISULFID 231 255
 FT DISULFID 247 268
 FT ACT_SITE 232 233
 FT CARBOHYD 144 144
 FT CARBOHYD 251 251
 FT CARBOHYD 261 261
 SQ SEQUENCE 302 AA; 34554 MW; F9AE82130A2A59f CRC64;

Query Match 6.5%; Score 11; DB 1; Length 302;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 FIYGGCRGN 144
 Db 81 FIYGGCRGN 91

RESULT 2

ISIK_HELP0 STANDARD; PRT; 58 AA.
 AC P00994;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE ISOINHIBITOR K.
 OS Helix pomatia (Roman snail) (Edible snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylommatophora;
 OC Helicoidae; Helicidae; Helix.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=76043680; PubMed=1183446;
 RX Tschesche H., Dietl T.;
 RT "The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequence determination by automated Edman degradation and mass-spectral identification of the phenylthiohydantoins.";
 RT Eur. J. Biochem. 58:439-451(1975).
 RL [2]

DISULFIDE BONDS.
 MEDLINE=76141310; PubMed=3462;

RA Dietl T., Tschesche H.;
 RT "The disulfide bridges of the trypsin-kallikrein inhibitor K from snails (Helix pomatia). Thermal inactivation and proteolysis by thermolysin.";
 RL Hoppe-Sevler's Z. Physiol. Chem. 357:139-145(1976).
 CC -1- FUNCTION: THIS IS ONE OF SEVERAL ISOINHIBITORS OF BROAD SPECIFICITY THAT ARE SECRETED INTO THE MUCUS OF THE SNAIL.
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.

DR PIR; A01223; TIRASK.
 DR HSSP; P00974; IRRB.
 DR INTERPRO; IPR002223;
 DR PFAM; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT_SITE 17 18
 SQ SEQUENCE 58 AA; 6451 MW; 6796586C488453B7 CRC64;

Query Match 5.3%; Score 9; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 FIYGGCRGN 142
 DB 35 FIYGGCRGN 43

RESULT 3

IVB3_VIPAA STANDARD; PRT; 65 AA.
 AC P00992;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE VENOM BASIC PROTEASE INHIBITOR III (VENOM CHYMOTRYPSIN INHIBITOR).
 OS Vipera ammodytes ammodytes (Western sand viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 RN [1]
 RP SEQUENCE.

RC TISSUE=VENOM;
 RA Ritonja A., Meloun B., Gubensek F.;
 RT "The primary structure of Vipera ammodytes venom chymotrypsin inhibitor.";
 RL Biochim. Biophys. Acta 746:138-145(1983).

CC -1- FUNCTION: THIS PROTEIN INHIBITS CHYMOTRYPSIN.
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR PIR; A01223; TIVIVC.
 DR HSSP; P31713; ISHP.

DR INTERPRO; IPR002223;
 DR PFAM; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Venom; Serine protease inhibitor.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT_SITE 17 18
 SQ SEQUENCE 65 AA; 7556 MW; 9D526F8E3BF7CC57 CRC64;

REACTIVE BOND (BY SIMILARITY).

Query Match 5.3%; Score 9; DB 1; Length 65;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 FIYGGCRGN 142
 DB 35 FIYGGCRGN 43

RESULT 4

COPE_YEAST STANDARD; PRT; 973 AA.

ID COPE_YEAST
 AC P41810; Q03779;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).
 GN SEC26 OR YDR238C OR YD8419.05C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.

RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=RSY255;
 RX MEDLINE=95014199; PubMed=7929113;
 RA Duden R., Hosobuchi M., Hamamoto S., Winsey M., Byers B., Schekman R.;

RT "Yeast beta- and beta'-coat proteins (COP). Two coatomer subunits
RT essential for endoplasmic reticulum-to-Golgi protein traffic.";
RL J. Biol. Chem. 269:24486-24495(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=288C / AB972;
RA Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIANE BIOSYNTHETIC
CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC TRANSPORT OF DILYSINE-TAGGED PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS
CC -!- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- MISCELLANEOUS: BREFELDIN A INDUCES DISSOCIATION FROM THE GOLGI OF
CC THE BETA-COP AND PRESUMABLY THE OTHER COATOMER SUBUNITS (BY
CC SIMILARITY).
CC -!- SIMILARITY: SIGNIFICANT, OF THE N-TERMINAL HALF OF BETA-COP WITH
CC THOSE OF BETA-ADAPTINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U11236; AAA61710.1; -;
DR EMBL; Z49701; CAA89724.1; -;
DR SGD; S0002646; SEC26.
*KW Transport; Protein transport; Golgi stack; Membrane; Phosphorylation.
FT CONFLICT 412 412 D -> E (IN REF. 1).
SQ SEQUENCE 973 AA; 109019 MW; 885420DB026BCFA3 CRC64;

Query Match 4.7%; Score 8; DB 1; Length 973;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 71 DLATSRNA 78
Db 347 DLATSRNA 354
|||||||

RESULT 5
YN81_CAEEL STANDARD; PRT; 1416 AA.
AC Q03610;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 316.1 KDA PROTEIN ZC84.1 IN CHROMOSOME III.
GN ZC84.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RC STRAIN=BRISTOL N2;
RA Jones S.J.M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: STRONG, TO D1044.3.
CC -!- SIMILARITY: CONTAINS 5 PROTEASE INHIBITOR DOMAINS BELONGING TO THE
CC BPTI/KUNITZ FAMILY OF INHIBITORS.
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CC -----
CC EMBL; Z19157; CAA79569.1; -;
DR PIR; S28291; S28291.
DR HSSP; P07204; ZADX.
DR WORMPEP; ZC84.1; CBI5020.
DR INTERPRO; IPR000561; -;
DR INTERPRO; IPR002223; -;
DR INTERPRO; IPR002899; -;
DR PFAM; PF01683; EB; 3.
DR PFAM; PF00014; Kunitz_BPTI; 5.
DR PRINTS; PR00759; BASICTPASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02279; BPTI_KUNITZ_2; 5.
DR PROSITE; PS01186; EGF_2; UNKNOWN.1.
KW Hypothetical protein; Serine protease inhibitor; Repeat.
FT DOMAIN 212 266 BPTI/KUNITZ INHIBITOR.
FT DOMAIN 352 387 BPTI/KUNITZ INHIBITOR.
FT DOMAIN 434 484 BPTI/KUNITZ INHIBITOR.
FT DOMAIN 538 590 BPTI/KUNITZ INHIBITOR.
FT DOMAIN 646 698 BPTI/KUNITZ INHIBITOR.
SQ SEQUENCE 1416 AA; 152986 MW; 531CACELCB22F70D CRC64;

Query Match 4.7%; Score 8; DB 1; Length 1416;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCDGNSNN 50
Db 572 GCDGNSNN 579
|||||||

RESULT 6
SBPI_SARBU STANDARD; PRT; 57 AA.
AC P26228;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PROTEASE INHIBITOR (SBPI).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Sarcophagidae; Sarcophaga.
[1]
RP SEQUENCE.
RC TISSUE=LARVAL HEMOLYMPH;
RX MEDLINE=93284121; PubMed=1304909;

RA Papayannopoulos I.A., Biemann K.;
 RT "Amino acid sequence of a protease inhibitor isolated from Sarcophaga
 RL bullata determined by mass spectrometry.";
 RL Protein Sci. 1:278-288(1992).
 CC -!- FUNCTION: SEEMS TO INHIBITS TRYPSIN.
 CC -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR PIR: A37294; A37294.
 DR INTERPRO: IPR002223; -.
 DR PFAM: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICPTASE.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 6 56 BY SIMILARITY.
 FT DISULFID 15 39 BY SIMILARITY.
 FT DISULFID 31 52 BY SIMILARITY.
 FT ACT_SITE 16 17 REACTIVE BOND (TRYPSIN) (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6518 MW; FC512C5399E87241 CRC64;

Query Match 4.1%; Score 7; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 YGCGRGN 142

|||||||

DB 36 YGCGRGN 42

RESULT 7

ID IBPI_TACTR STANDARD; PRT; 61 AA.
 AC P16044;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE PROTEINASE INHIBITOR (BPTI-TYPE).
 OS Tachypleus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachypleus.
 RN [1]

SEQUENCE.

RC TISSUE=HEMOCYTE;
 RX MEDLINE=88007472; PubMed=3308864;
 RA Nakamura T., Hirai T., Tokunaga F., Kawabata S., Iwanaga S.;
 RT "Purification and amino acid sequence of Kunitz-type protease
 RT inhibitor found in the hemocytes of horseshoe crab (Tachypleus
 RT tridentatus).";
 CC -!- FUNCTION: INHIBITOR OF TRYPSIN AND CHYMOTRYPSIN.
 CC -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.

DR PIR: A26923; A26923.

DR HSSP: P00974; 4TPI.

DR INTERPRO: IPR002223; -.
 DR PFAM: PF00014; Kunitz_BPTI; 1.

DR PRINTS: PR00759; BASICPTASE.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.

KW Serine protease inhibitor.

FT DISULFID 8 58 BY SIMILARITY.

FT DISULFID 17 41 BY SIMILARITY.

FT DISULFID 33 54 BY SIMILARITY.

FT ACT_SITE 18 19 REACTIVE BOND (BY SIMILARITY).

SQ SEQUENCE 61 AA; 6825 MW; 730E82CDD0653E48 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 VTGPCRA 117

|||||||

DB 13 VTGPCRA 19

RESULT 8

ID IVBT_ERIMA STANDARD; PRT; 62 AA.
 AC P24541;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE VENOM TRYPSIN INHIBITOR.
 OS Eristocophis macmahoni (Leaf-nosed viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Eristocophis.
 RN [1]

SEQUENCE.

RC TISSUE=VENOM;

RX MEDLINE=92077130; PubMed=1743283;

RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;

RT "Purification and characterization of a Kunitz-type trypsin inhibitor

RT from Leaf-nosed viper venom.";

RL FEBS Lett. 294:141-143(1991).

CC -!- FUNCTION: THIS PROTEIN INHIBITS TRYPSIN AND KALLIKREIN.

CC -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.

DR PIR: S19327; S19327.

DR HSSP: P31713; 1SHP.

DR INTERPRO: IPR002223; -.
 DR PFAM: PF00014; Kunitz_BPTI; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.

KW Venom; Serine protease inhibitor.

FT DISULFID 2 52 BY SIMILARITY.

FT DISULFID 11 35 BY SIMILARITY.

FT DISULFID 27 48 BY SIMILARITY.

FT ACT_SITE 12 13 REACTIVE BOND (BY SIMILARITY).

SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 NFYGGC 139

|||||||

DB 29 NFYGGC 35

RESULT 9

ID NLTP_DAUCA STANDARD; PRT; 120 AA.
 AC P27631;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (EXTRACELLULAR
 DE PROTEIN 2).
 GN EP2.
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
 OC euasterids II; Apiales; Apiaceae; Daucus.
 RN [1]

RC STRAIN=CV. NORTHRUP KING;

RX MEDLINE=92361243; PubMed=1822991;

RA Sterk P., Booldj H., Scheellekens G.A., van Kammen A., de Vries S.C.;

RT "Cell-specific expression of the carrot EP2 lipid transfer protein

RT gene.";

RL Plant Cell 3:907-921(1991).

CC -!- FUNCTION: PLANT NONSPECIFIC LIPID-TRANSFER PROTEINS TRANSFER

CC PHOSPHOLIPIDS AS WELL AS GALACTOLIPIDS ACROSS MEMBRANES. MAY PLAY

CC A ROLE IN WAX OR CUTIN DEPOSITION IN THE CELL WALLS OF EXPANDING

CC EPIDERMAL CELLS AND CERTAIN SECRETORY TISSUES.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN PROTODERM CELLS OF SOMATIC AND
 CC ZYGOTIC EMBRYOS, AND TRANSIENTLY EXPRESSED IN EPIDERMAL CELL
 CC LAYERS OF LEAVES, FLOWERS, AND SEEDS.
 CC -!- SIMILARITY: BELONGS TO THE PLANT LTP FAMILY.
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 CC -----
 CC EMBL; M64746; AAB96834.1; -;
 CC PIR; JQ1280; JQ1280.
 CC HSSP; P19656; IAEH.
 CC INTERPRO: IPR000528; -;
 CC PFAM; PF00279; LTP; 1.
 CC PRINTS; PR00382; LIPIDTRNSFR.
 CC PROSITE; PS00597; PLANT_LTP; 1.
 CC Lipid-binding; Transport; Signal.
 CC SIGNAL 1 26 POTENTIAL.
 CC CHAIN 27 120 NONSPECIFIC LIPID-TRANSFER PROTEIN.
 CC DISULFID 30 79 BY SIMILARITY.
 CC DISULFID 40 56 BY SIMILARITY.
 CC DISULFID 57 102 BY SIMILARITY.
 CC DISULFID 77 116 BY SIMILARITY.
 CC DISULFID 120 AA; 12504 MW; E85C6EBA5E592214 CRC64;
 CC SEQUENCE

Query Match 4.1%; Score 7; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 TANAVTG 113
 DB 83 TANAVTG 89

RESULT 10
 IATR_HORSE STANDARD; PRT; 123 AA.
 AC P04365;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE INTER-ALPHA-TRYPsin INHIBITOR (ITI) (HI-14) (INHIBITORY FRAGMENT OF
 ITI) (FRAGMENT).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-85225967; PubMed-2408637;
 RA Hochstrasser K., Wächter E., Albrecht G.J., Reisinger P.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
 RT the inter-alpha-trypsin inhibitor, X. The amino acid sequences of the
 RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
 RT inhibitors.";
 RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
 CC -!- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER
 CC LIMITED PROTEOLYSIS WITH TRYPsin, CONTAINS TWO HOMOLOGOUS DOMAINS.
 CC WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPsin, THE
 CC FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND
 CC NOT AT ALL WITH PANCREATIC ELASTASE.
 CC -!- MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO
 CC DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.
 CC INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH
 CC CHYMOTRYPsin AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.
 CC -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 CC PIR; A01210; TH0B1.
 CC HSSP; P10646; IADZ.

DR INTERPRO: IPR002223; -;
 DR PFAM; PF00014; Kunitz_BPTI; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 KW Plasma; Glycoprotein; Serine protease inhibitor; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 1 56 I.
 FT DOMAIN 57 123 II.
 FT DISULFID 5 55
 FT DISULFID 14 38
 FT DISULFID 30 51
 FT DISULFID 61 111
 FT DISULFID 70 94
 FT DISULFID 86 107
 FT ACT_SITE 15 16 INHIBITORY SITE (P1) (CHYMOTRYPsin,
 ELASTASE).
 FT ACT_SITE 71 72 INHIBITORY SITE (P1) (TRYPsin).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. .).
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13510 MW; CE1A9120774411D5 CRC64;
 SEQUENCE

Query Match 4.1%; Score 7; DB 1; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 YGCGRGN 142
 DB 91 YGCGRGN 97

RESULT 11
 TRPE_BUCAI STANDARD; PRT; 521 AA.
 AC Q44695;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
 GN TRPE OR BUPT01.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OG Plasmid pBAP.
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96215866; PubMed-8642610;
 RA Rounbakhsh D., Cai C.-Y., von Dohlen C.D., Clark M.A., Baumann L.,
 RA Baumann P., Moran N.A., Voegtlin D.J.;
 RT "The tryptophan biosynthetic pathway of aphid endosymbionts
 RT (Buchnera): genetics and evolution of plasmid-associated anthranilate
 RT synthase (trpEG) within the aphididae.";
 RL J. Mol. Evol. 42:414-421(1996).
 CC -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
 CC PYRUVATE + L-GLUTAMATE.
 CC -!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN
 CC -!- SUBUNIT: Tetramer of two components I and two components II (B;
 CC SIMILARITY).
 CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
 CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
 CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
 CC FAMILY.
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 CC -----
 CC EMBL; L43555; AAD09346.1; -;

DR PRAM: PF00425; chorismate_bind; 1.
DR PRINS: PRO0095; ANTSNTHASEI.
KW Tryptophan biosynthesis; Lyase; Plasmid.
SQ SEQUENCE 521 AA; 56695 MW; 2855F8FE7DF4271 CRC64;

Query Match 4.1%; Score 7; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 12 LVSKVG 18
| | | | | | | |
DB 400 LVSKVG 406

RESULT 12
CO3_HUMAN
ID CO3_HUMAN STANDARD; PRT; 1663 AA.
AC P01024;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
RT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
FE COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN].
GN C3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RA "Human complement component C3: cDNA coding sequence and derived primary structure.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:708-712(1985).
RN [2]
RP SEQUENCE OF 672-748.
RX MEDLINE=76069169; PubMed=1238393;
RA Hugli T.E.;
RT "Human anaphylatoxin (C3a) from the third component of complement. Primary structure.";
RL J. Biol. Chem. 250:8293-8301(1975).
RN [3]
RP SEQUENCE OF 1409-1563.
RX MEDLINE=88154452; PubMed=3279119;
RA Daoudaki M.B., Becherer J.D., Lambiris J.D.;
RT "A 34-amino acid peptide of the third component of complement mediates properdin binding.";
RL J. Immunol. 140:1577-1580(1988).
RN [4]
RP SEQUENCE OF 988-1036.
RX MEDLINE=82174534; PubMed=6175959;
RA Thomas M.L., Janatova J., Gray W.R., Tack B.F.;
RT "Third component of human complement: localization of the internal thioester bond.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1054-1058(1982).
RN [5]
RP STRUCTURE BY NMR OF C3A.
RX MEDLINE=88276894; PubMed=3260670;
RA Nettlesheim D.G., Edalji R.P., Mollison K.W., Greer J., Zuiderweg E.R.;
RT "Secondary structure of complement component C3a anaphylatoxin in solution as determined by NMR spectroscopy: differences between crystal and solution conformations.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5036-5040(1988).
RN [6]
RP MUTAGENESIS OF THIOESTER BOND REGION.
RX MEDLINE=92250565; PubMed=1577777;
RA Isaac L., Isenman D.E.;
RT "Structural requirements for thioester bond formation in human complement component C3. Reassessment of the role of thioester bond integrity on the conformation of C3.";
RL J. Biol. Chem. 267:10062-10069(1992).
RN [7]
RP DISULFIDE BONDS.

RX MEDLINE=93106233; PubMed=8416818;
RA Dolner K., Sottrup-Jensen L.;
RT "Disulfide bridges in human complement component C3b.";
RL FEBS Lett. 315:85-90(1993).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 996-1303.
RX MEDLINE=98259089; PubMed=9596584;
RA Nagar B., Jones R.G., Diefenbach R.J., Isenman D.E., Rini J.M.;
RT "X-ray crystal structure of C3d: a C3 fragment and ligand for complement receptor 2.";
RL Science 280:1277-1281(1998).
RN [9]
RP VARIANT C3F/S.
RX MEDLINE=89309808; PubMed=2473125;
RA Pozhansky M.C., Clissold P.M., Lachmann P.J.;
RT "The difference between human C3f and C3s results from a single amino acid change from an asparagine to an aspartate residue at position 1216 on the alpha-chain of the complement component, C3.";
RL J. Immunol. 143:1254-1258(1989).
RN [10]
RP ERRATUM (RETRACTION OF ABOVE ARTICLE).
RX MEDLINE=90063087; PubMed=2584723;
RA Pozhansky M.C., Clissold P.M., Lachmann P.J.;
RL J. Immunol. 143:3860-3862(1989).
RN [11]
RP VARIANTS G1Y-102 AND PRO-314.
RX MEDLINE=9101240; PubMed=1976733;
RA Botto M., Yong Fong K., So A.K., Koch C., Walport M.J.;
RT "Molecular basis of polymorphisms of human complement component C3.";
RL J. Exp. Med. 172:1011-1017(1990).
RN [12]
RP VARIANT ASN-549.
RX MEDLINE=95050640; PubMed=7961791;
RA Singer L., Whitehead W.T., Akama H., Katz Y., Fishelson Z., Wetzel R.A.;
RT "Inherited human complement C3 deficiency. An amino acid substitution in the beta-chain (ASP549 to ASN) impairs C3 secretion.";
RL J. Biol. Chem. 269:28494-28499(1994).
RN [13]
RP VARIANT GLN-1320.
RA Watanabe Y., Matsui N., Yan K., Nishimukai H., Tokunaga K., Juji T., Kobayashi N., Kohsaka T.;
RT "A novel C3 allotype C3/F02 has an amino acid substitution that may inhibit iC3b synthesis and cause C3-hypocomplementemia.";
RL Mol. Immunol. 30:62-62(1993).
CC -!- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUKOCYTES.
CC -!- SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 APC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN, RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA' CHAIN).
CC -!- POLYMORPHISM: THERE ARE TWO ALLELES: C3S (C3 SLOW), THE MOST COMMON ALLELE IN ALL RACES AND C3F (C3 FAST), RELATIVELY FREQUENT IN CAUCASIIDS, LESS COMMON IN BLACK AMERICAN, EXTREMELY RARE IN ORIENTALS.
CC -!- DISEASE: C3 DEFICIENCY CAUSES A SUSCEPTIBILITY TO PYOGENIC INFECTION.
CC -!- MISCELLANEOUS: C3B IS RAPIDLY SPLIT IN TWO POSITIONS BY FACTOR T AND A COFACTOR TO FORM IC3B (INACTIVATED C3B) AND C3F WHICH IS RELEASED.
CC -!- MISCELLANEOUS: IC3B IS THE SLOWLY CLEAVED (POSSIBLY BY FACTOR I) TO FORM C3C AND C3DG. OTHER PROTEASES PRODUCE OTHER FRAGMENTS SUCH AS C3D OR C3G.
CC -!- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.

!-!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.

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Query Match	Score 7	DB 1	Length 1663
EMBL; K02765; AAA05332.1; -	549	4.1%	Score 7; DB 1; Length 1663;
PIR: A01257; C3HU.	314		
PIR: A27603; A27603.	549		
PDB: 1C3D; 18-NOV-98.	314		
SWISS-2DPAGE; P01024; HUMAN.	549		
MIN; 120700; -	314		
INTERPRO; IPR000020; -	549		
INTERPRO; IPR001134; -	314		
INTERPRO; IPR001599; -	549		
INTERPRO; IPR001840; -	314		
INTERPRO; IPR002890; -	549		
PFAM; PF00207; A2M; 1.	314		
PFAM; PF01835; A2M; N; 1.	549		
PFAM; PF01821; ANATO; 1.	314		
PFAM; PF01759; NTR; 1.	549		
PRINTS; PR00004; ANAPHYLATOXN.	314		
PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.	549		
PROSITE; PS01177; ANAPHYLATOXIN_1; 1.	314		
PROSITE; PS01178; ANAPHYLATOXIN_2; 1.	549		
Complement pathway; Complement alternate pathway; Plasma;			
Inflammatory response; Glycoprotein; Signal; Polymorphism;			
Disease mutation; 3D-structure.			
SIGNAL 1 22			
CHAIN 23 1663			
COMPLEMENT C3.			
CHAIN 23 667			
COMPLEMENT C3, BETA CHAIN.			
CHAIN 672 1663			
COMPLEMENT C3, ALPHA CHAIN.			
PEPTIDE 672 748			
CHAIN 749 1663			
C3A ANAPHYLATOXIN.			
CHAIN 749 1663			
C3B ALPHA' CHAIN.			
PEPTIDE 749 934			
CHAIN 935 1303			
C3C FRAGMENT.			
PEPTIDE 935 1001			
CHAIN 1002 1303			
C3D FRAGMENT.			
PEPTIDE 1002 1303			
CHAIN 1304 1320			
C3F FRAGMENT.			
PEPTIDE 748 749			
CHAIN 954 955			
CLEAVAGE (BY C3 CONVERTASE).			
SITE 954 955			
CHAIN 1302 1304			
CLEAVAGE (BY FACTOR I).			
SITE 1302 1321			
CHAIN 693 728			
CLEAVAGE (BY FACTOR I).			
DOMAIN 1424 1456			
ANAPHYLATOXIN-LIKE.			
PROPERDIN-BINDING.			
INTERCHAIN.			
DISULFID 559 816			
CHAIN 627 662			
DISULFID 627 662			
CHAIN 693 720			
DISULFID 694 727			
CHAIN 707 728			
DISULFID 707 728			
CHAIN 873 1513			
DISULFID 873 1513			
CHAIN 1101 1158			
DISULFID 1101 1158			
CHAIN 1358 1489			
DISULFID 1358 1489			
CHAIN 1389 1458			
DISULFID 1389 1458			
CHAIN 1506 1511			
DISULFID 1506 1511			
CHAIN 1518 1590			
DISULFID 1518 1590			
CHAIN 1537 1661			
DISULFID 1537 1661			
CHAIN 1637 1646			
DISULFID 1637 1646			
CHAIN 85 85			
CARBOHYD 85 85			
CHAIN 939 939			
CARBOHYD 939 939			
CHAIN 1617 1617			
CARBOHYD 1617 1617			
CHAIN 1010 1013			
THIOLEST 1010 1013			
CHAIN 102 102			
R -> G (IN ALLELE C3F).			
FTID=VAR_001983.			
L -> P.			
D -> N (IN C3 DEFICIENCY; IMPAIRS			
FTID=VAR_001984.			
Variant 314 314			
Variant 549 549			

Best Local Similarity 100.0%; Pred. NO. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 46 GNSNNYL 52
|||||
DB 450 GNSNNYL 456

RESULT 13
LRP2_RAT
ID LRP2_RAT STANDARD; PRT; 4560 AA.
AC P98158;
DC DT 01-OCT-1996 (Rel. 34, Created)
DT DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
DE DE (GLYCOPROTEIN 330).
GN LRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; [M]
RC SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
RX MEDLINE=95024033; PubMed=7937880;
RA Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.;
RT "Complete cloning and sequencing of rat gp330/'megalin,' a
RT distinctive member of the low density lipoprotein receptor gene
RT family";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).
RN [2]
RN FUNCTION.
RX MEDLINE=95386696; PubMed=7544804;
RA Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,
RA Norris K., Gliemann J., Christensen E.I.;
RT "Evidence that epithelial glycoprotein 330/megalin mediates uptake of
RT polybasic drugs.";
RL J. Clin. Invest. 96:1404-1413(1995).
RN [3]
RN TISSUE SPECIFICITY.
RX MEDLINE=94172242; PubMed=7510321;
RA Zheng G., Bachinsky R.T., Stamenkovic I., Strickland D.K., Brown D.,
RA Andres G., McCluskey R.J.;
RT "Organ distribution in rats of two members of the low-density
RT lipoprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
RT receptor-associated protein (RAP)";
RL J. Biochem. Cytochem. 42:531-542(1994).
CC -!- FUNCTION: BINDS PLASMINOGEN EXTRACELLULAR MATRIX COMPONENTS,
CC PLASMINOGEN ACTIVATOR-PLASMINOGEN ACTIVATOR INHIBITOR TYPE I
CC COMPLEX, APOLIPOPROTEIN E-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
CC LACTOFERRIN, CLUSTERIN AND CALCIUM.
CC -!- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS
CC APRONITIN, AMINOGLYCOSIDES AND POLYMYXIN B.
CC -!- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-
CC ASSOCIATED PROTEIN (RAP).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXPRESSED IN
CC CLATHRIN-COATED PITS; A SOLUBLE FORM IS POSSIBLY DERIVED BY
CC CLEAVAGE AT THE CELL SURFACE.
CC -!- TISSUE SPECIFICITY: EPITHELIAL CELLS OF KIDNEY GLOMERULUS AND
CC PROXIMAL TUBULE, LUNG, EPIDIDYMIS, YOLK SAC, AMONG OTHERS.
CC -!- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.
CC -!- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
CC -!- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 SH3-BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to licens@isb-sib.ch).

RESULT 14
ISF2_GALME
ID ISF2_GALME STANDARD; PRT; 52 AA.
AC P81906;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INDUCIBLE SERINE PROTEASE INHIBITOR 2 (ISPI-2) (FRAGMENT).
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Pyraloidea; Pyralidae; Galleriinae; Galleria.
RN [1]
PC SEQUENCE.
RP TISSUE=HEMOLYMPH;
RX MEDLINE=20193629; PubMed=10727944;
RA Froebius A.C., Kanost M.R., Goetz P., Vilcinskis A.;
RT "Isolation and characterization of novel inducible serine protease
inhibitors from larval hemolymph of the greater wax moth Galleria
mellonella";
RL Eur. J. Biochem. 267:2046-2053(2000).
CC -!- FUNCTION: INHIBITS TRYPSIN AND THE TOXIN PROTEASE PR2 OF M.
CC ANISOPLIAE. DOES NOT INHIBIT CHYMOTRYPSIN, SUBTILISIN CARLSBERG,
CC PROTEINASE K, PORCINE PANCREATIC ELASTASE AND THE TOXIN PROTEASE
CC PR1 OF M. ANISOPLIAE.
CC -!- DEVELOPMENTAL STAGE: LAST INSTAR LARVAE.
CC -!- INDUCTION: BY INFECTION.
CC -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR INTERPRO: IPR002223; -.
DR PFAM: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
-DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 6057 MW; 31CED34D59C42ABE CRC64;

Query Match 3.5%; Score 6; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 FVYGGC 44
|||||
33 FVYGGC 38

RESULT 15
ISH1_STOHE
ID ISH1_STOHE STANDARD; PRT; 55 AA.
AC P31713;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE KUNITZ-TYPE PROTEINASE INHIBITOR SHPI-1
OS Stoichactis helianthus (Caribbean sea anemone) (Stichodactyla
helianthus).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Stichodactylidae; Stichodactyla.
RN [1]
PC SEQUENCE.
RX MEDLINE=97179757; PubMed=9027993;
RA Delfin J., Martinez I., Antuch W., Morera V., Gonzalez Y.,
RA Rodriguez R., Marquez M., Saroyan A., Larionova N., Diaz J.,
RA Padron G., Chavez M.;
RT "Purification, characterization and immobilization of proteinase
inhibitors from Stichodactyla helianthus";
RL Toxicon 34:1367-1376(1996).
RN [2]

RP STRUCTURE BY NMR, AND DISULFIDE BONDS.
RX MEDLINE=93215644; PubMed=8462542;
RA Antuch W., Berndt K.D., Chavez M.A., Delfin J., Wuethrich K.;
RT "The NMR solution structure of a Kunitz-type proteinase inhibitor
from the sea anemone Stichodactyla helianthus";
RL Eur. J. Biochem. 212:675-684(1993).
CC -!- FUNCTION: ACTIVE AGAINST SERINE, CYSTEINE, AND ASPARTIC
CC PROTEINASES.
CC -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR PIR: S30332; S30332.
DR PDB: 1SHP; 31-JAN-94.
DR INTERPRO: IPR002223; -.
DR PFAM: PF00014; Kunitz_BPTI; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; 3D-structure.
FT DISULFID 3 53
FT DISULFID 12 36
FT DISULFID 28 49
FT ACT_SITE 13 14
FT HELIX 2 4
FT STRAND 17 22
FT TURN 23 26
FT STRAND 27 32
FT TURN 36 37
FT STRAND 43 43
FT HELIX 46 53
SQ SEQUENCE 55 AA; 6116 MW; 532B96E3127000D4 CRC64;

Query Match 3.5%; Score 6; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 FVYGGC 139
|||||
Db 31 FVYGGC 36

Search completed: January 31, 2001, 15:07:48
Job time: 116 sec

Wed Jan 31 15:14:33 2001

us-09-441-654a-1.oli.rsp

Page 10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:05:23 ; Search time 22.96 Seconds
(without alignments)
867.829 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 170
Sequence: 1 ADERSIHDFCLVSKVVGRC.....ACMLRCFROQENPPLGLSK 170

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Ed size: 0

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: SPREMBL15.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_phase.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_vertebrate.*
15: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	252	4	O43291
2	170	100.0	252	4	O00271
3	144	84.7	252	4	O14895
4	13	7.6	195	11	O9WU04
5	13	7.6	252	11	O9WU03
6	9	5.3	58	5	O9TWG0
7	9	5.3	58	5	O9TWG9
8	8	4.7	59	5	O9TWG8
9	8	4.7	922	5	O21418
10	8	4.7	1195	5	O9N343
11	8	4.7	1599	5	O09983
12	7	4.1	110	5	O9VQU0
13	7	4.1	183	5	O16784
14	7	4.1	210	13	O91443
15	7	4.1	230	13	O13000
16	7	4.1	253	2	O54224
17	7	4.1	260	5	O46164
18	7	4.1	355	5	O9VQ08
19	7	4.1	438	4	O9Y4N9

20	7	4.1	499	2	Q9L2G7	Q9L2G7 streptomyce
21	7	4.1	500	2	Q9ZN02	Q9ZN02 helicobacte
22	7	4.1	507	2	O87080	O87080 vibrio chol
23	7	4.1	514	5	O9TWE5	O9TWE5 carcinoscor
24	7	4.1	521	2	O9KGQ2	O9KGQ2 buchnera sp
25	7	4.1	521	5	O9W3R0	O9W3R0 drosophila
26	7	4.1	654	5	O9VFX6	O9VFX6 drosophila
27	7	4.1	719	5	O9U021	O9U021 giardia lam
28	7	4.1	719	5	O9U019	O9U019 giardia lam
29	7	4.1	763	5	O9XZD0	O9XZD0 drosophila
30	7	4.1	836	4	O94856	O94856 homo sapien
31	7	4.1	972	5	O44938	O44938 haemochus
32	7	4.1	974	13	O91735	O91735 xenopus lae
33	7	4.1	988	13	Q07498	Q07498 gallus gall
34	7	4.1	1151	11	Q9QVNS	Q9QVNS rattus sp.
35	7	4.1	1214	5	Q25338	Q25338 latrodectus
36	7	4.1	1474	5	O62504	O62504 caenorhabdi
37	7	4.1	1668	4	O15026	O15026 homo sapien
38	7	4.1	1787	10	O9SJP0	O9SJP0 arabidopsis
39	7	4.1	2167	5	O76840	O76840 caenorhabdi
40	7	4.1	2208	5	Q09515	Q09515 caenorhabdi
41	7	4.1	2230	5	Q9WAV4	Q9WAV4 drosophila
42	7	4.1	2971	4	Q9X5L9	Q9X5L9 homo sapien
43	7	4.1	3198	5	Q9U8G8	Q9U8G8 mangusta
44	6	3.5	41	12	O11552	O11552 mus muscu
45	6	3.5	42	2	Q49201	Q49201 myoblast

ALIGNMENTS

RESULT 1
O43291
ID O43291 PRELIMINARY; PRT; 252 AA.
AC O43291;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98010584; PubMed=9346890;
RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,
RA Kitamura N.;
RT *Purification and cloning of hepatocyte growth factor activator
RT inhibitor type 2, a Kunitz-type serine protease inhibitor.";
RL J. Biol. Chem. 272:27558-27564(1997).
DR EMBL; AB006534; BAA25024.1; -.
DR HSP; P05067; ITAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Serine protease inhibitor.
SQ SEQUENCE 252 AA; 28189 MW; F7D3D834ED631DF0 CRC64;

Query Match 100.0%; Score 170; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADERSIHDFCLVSKVVGRCASMPRWNTVTDGSCQLFVYGGCDGNSNLYLKECLKK 60
Db 28 ADERSIHDFCLVSKVVGRCASMPRWNTVTDGSCQLFVYGGCDGNSNLYLKECLKK 87
Qy 61 CATVTENATGDLATSRNAADSSVPSAPRQDSEHSSDMFNVEEYCTANAVTGPCRASFP 120
Db 88 CATVTENATGDLATSRNAADSSVPSAPRQDSEHSSDMFNVEEYCTANAVTGPCRASFP 147

01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.
 GN HAI2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C.
 RX MEDLINE=99160423; PubMed=10049781;
 RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
 RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
 Kunitz-type serine proteinase inhibitor domain is a predominant
 product in mouse but not in human."
 RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
 DR EMBL: AF099016; AAD2172.1; -.
 DR HSSP: P05067; ITAW.
 DR INTERPRO: IPR002223; -.
 DR PFAM: PF00014; Kunitz_BPTI; 2.
 DR PRINTS: PR00759; BASICTPASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 2.
 KW Serine protease inhibitor.
 SQ SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;

Query Match 7.6%; Score 13; DB 11; Length 252;
 Best Local Similarity 100.0%; Pred. No. 4.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 FIYGGCRGNKNSY 146
 Db 161 FIYGGCRGNKNSY 173
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RESULT 6
 Q9TWF8
 ID Q9TWF8 PRELIMINARY; PRT; 58 AA.
 AC Q9TWF8
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE KALICLUDINE 1, ASKC1.
 DE KALICLUDINE 1, ASKC1.
 OS Anemonia sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynantheae; Actiniidae; Anemonia.
 OX NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96027617; PubMed=7559645;
 RA Schweitz H., Bruhn T., Guillemaire E., Moinier D., Lancelin J.M.,
 RA Beress L., Lazdunski M.;
 RT "Kalicludines and kaliseptine. Two different classes of sea anemone
 toxins for voltage sensitive K+ channels."
 RL J. Biol. Chem. 270:25121-25126(1995).
 DR HSSP: P10646; 1ADZ.
 DR INTERPRO: IPR002223; -.
 DR PFAM: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 1.
 SQ SEQUENCE 58 AA; 6691 MW; 253E068896B4BD8D CRC64;

Query Match 5.3%; Score 9; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 FIYGGCRGN 142
 Db 33 FIYGGCRGN 41
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RESULT 7

Q9TWF9
 ID Q9TWF9 PRELIMINARY; PRT; 58 AA.
 AC Q9TWF9
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE KALICLUDINE 2, ASKC2.
 OS Anemonia sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynantheae; Actiniidae; Anemonia.
 OX NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96027617; PubMed=7559645;
 RA Schweitz H., Bruhn T., Guillemaire E., Moinier D., Lancelin J.M.,
 RA Beress L., Lazdunski M.;
 RT "Kalicludines and kaliseptine. Two different classes of sea anemone
 toxins for voltage sensitive K+ channels."
 RL J. Biol. Chem. 270:25121-25126(1995).
 DR HSSP: P12111; 2KNT.
 DR INTERPRO: IPR002223; -.
 DR PFAM: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 1.
 SQ SEQUENCE 58 AA; 6778 MW; F102E71682F1A55C CRC64;

Query Match 5.3%; Score 9; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 FIYGGCRGN 142
 Db 33 FIYGGCRGN 41
 |||||

RESULT 8
 Q9TWF8
 ID Q9TWF8 PRELIMINARY; PRT; 59 AA.
 AC Q9TWF8
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE KALICLUDINE 3, ASKC3.
 OS Anemonia sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynantheae; Actiniidae; Anemonia.
 OX NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96027617; PubMed=7559645;
 RA Schweitz H., Bruhn T., Guillemaire E., Moinier D., Lancelin J.M.,
 RA Beress L., Lazdunski M.;
 RT "Kalicludines and kaliseptine. Two different classes of sea anemone
 toxins for voltage sensitive K+ channels."
 RL J. Biol. Chem. 270:25121-25126(1995).
 DR HSSP: P31713; 1SHP.
 DR INTERPRO: IPR002223; -.
 DR PFAM: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR PROSITE: PS00280; BPTI_KUNITZ; 1.
 SQ SEQUENCE 59 AA; 6738 MW; 0C7695C3F394D4A5 CRC64;

Query Match 4.7%; Score 8; DB 5; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KVVGCRGA 22
 Db 9 KVVGCRGA 16
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```
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024830; AAF59608.1; -.
SQ SEQUENCE 1195 AA; 131342 MW; E77C3A6DF2272A18 CRC64;

Query Match 4.7%; Score 8; DB 5; Length 1195;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCDGNSNN 50
DB 887 GCDGNSNN 894

RESULT 11
Q09983 PRELIMINARY; PRT; 1599 AA.
ID Q09983
AC Q09983;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 171.7 KDA PROTEIN F30H5.3 IN CHROMOSOME III.
GN F30H5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Pauley A., Steeves L.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO C.ELEGANS ZC84.1.
CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR EMBL; U29096; AAA68408.1; -.
DR HSP; P10646; 1TFX.
DR WORMPEP; F30H5.3; CE01927.
DR INTERPRO; IPR002198; -.
DR INTERPRO; IPR002223; -.
DR INTERPRO; IPR002899; -.
DR PFAM; PF00014; Kunitz_BPTI; 6.
DR PFAM; PF01683; EB; 3.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Hypothetical protein; Serine protease inhibitor.
FT DOMAIN 7. 10 POLY-LEU.
FT DOMAIN 1520 1523 POLY-GLU.
SQ SEQUENCE 1599 AA; 171658 MW; AB5E6A1D86E9880D CRC64;

Query Match 4.7%; Score 8; DB 5; Length 1599;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCDGNSNN 50
DB 704 GCDGNSNN 711

RESULT 12
Q09VQ0 PRELIMINARY; PRT; 110 AA.
ID Q09VQ0
AC Q09VQ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

RT "Genome sequence of the nematode C. elegans: a platform for
```

DE CG10031 PROTEIN.
 GN CG10031.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Nephelidae; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jalali M., Kalush F., Karpen G.H., Ji J., Wei M.-H., Ibegwam C.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Merkulov G., Milshina N.V., Mobarly B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Mount S.M., Moy M., Murphy K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 Science 287:2185-2193(2000).
 EMBL; AE003579; AAF51074.1; -.
 HSSP; P12111; 2KNT.
 DR FLXBASE; FBgn0031563; CG10031.
 DR INTERPRO; IPR002223; -.
 DR PFAM; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPRASE.
 SQ SEQUENCE 110 AA; 12240 MW; BB3F2DF4A7EF509D CRC64;

Query Match 4.1%; Score 7; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 YGGCRGN 142
 Db 86 YGGCRGN 92
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RESULT 13
 OL6784
 ID OL6784 PRELIMINARY; PRT; 183 AA.
 AC OL6784;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DR EMBL; Z50082; CAA90413.1; -.
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE SIMILAR TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 GN T21D12.12.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Willson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Woessner J.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016687; AAC48097.1; -.
 DR HSSP; P10646; 1TFX.
 DR INTERPRO; IPR002223; -.
 DR PFAM; PF00014; Kunitz_BPTI; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ; 1.
 KW Serine protease inhibitor.
 SQ SEQUENCE 183 AA; 20143 MW; CCBE4BE2293CE32A CRC64;

Query Match 4.1%; Score 7; DB 5; Length 183;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCDGNSN 49
 Db 58 GCDGNSN 64
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RESULT 14
 Q91443
 ID Q91443 PRELIMINARY; PRT; 210 AA.
 AC Q91443;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 OS INSULIN-LIKE GROWTH FACTOR II PRECURSOR.
 CC Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 CC Elasmobranchii; Squala; Squalidae; Squalus.
 NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=95394151; PubMed=7545136;
 RA Duguay S.J., Chan S.J., Mommensen T.P., Steiner D.F.;
 RT "Divergence of insulin-like growth factors I and II in the
 elasmobranch, Squalus acanthias.";
 RL FEBS Lett. 371:59-72(1995).
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; Z50082; CAA90413.1; -.
 DR HSSP; P01344; 1GF2.
 DR INTERPRO; IPR000739; -.
 DR PFAM; PF00049; Insulin; 1.

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Wed Jan 31 15:14:34 2001

DR PRINTS: PR00276; INSULINA.
 DR PRINTS: PR00277; INSULINB.
 DR PROSITE: PS00262; INSULIN; 1.
 DR PRODOM: PD001048; -; 1.
 KW SIGNAL. 1 49 POTENTIAL.
 FT SIGNAL 50 210 INSULIN-LIKE GROWTH FACTOR II.
 FT CHAIN 50 210
 FT SEQUENCE 210 AA; 23027 MW; 9B433B7C4749A03A CRC64;
 SQ

Query Match 4.1%; Score 7; DB 13; Length 210;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VSKVGR 19
 DB 78 VSKVGR 84

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 AC 013000;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE PROTEASOME SUBUNIT Y (EC 3.4.99.46).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Nonaka M., Namikawa C., Sasaki M., Salter-Cid L., Flajnik M.F.;
 RL J. Immunol. 0:0-0(0).
 DR EMBL; D87689; BAA19760.1; -.
 DR MEROPS; T01.010; -.
 DR INTERPRO; IPR000243; -.
 DR INTERPRO; IPR001353; -.
 DR PFAM; PF00227; proteasome; 1.
 DR PRINTS; PR00141; PROTEASOME.
 DR PROSITE; PS00854; PROTEASOME.B; 1.
 KW Proteasome; Hydrolase; Protease.
 SQ SEQUENCE 230 AA; 24553 MW; 2A1C9B3494473D87 CRC64;

Query Match 4.1%; Score 7; DB 13; Length 230;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TRECLK 59
 DB 178 TRECLK 184

Search completed: January 31, 2001, 15:07:35
 Job time: 132 sec

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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:04:19 ; Search time 15.92 Seconds
(without alignments)
191.752 Million cell updates/sec

Title: US-09-441-654A-1

Perfect score: 170

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Scoring table:

Gapop 60.0 , Gapext 60.0

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File size : 0

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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5: /cgn2.6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	170	100.0	252	1	US-08-974-196-7
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4	26	15.3	26	2	US-08-974-196-3
5	15	8.8	29	1	US-08-685-660A-2
6	15	8.8	29	2	US-08-974-196-2
7	10	5.9	15	1	US-08-685-660A-1
8	10	5.9	15	2	US-08-974-196-1
9	10	5.9	58	3	US-08-676-124-93
10	10	5.9	58	3	US-08-676-124-103
11	10	5.9	58	3	US-09-414-878-93
12	10	5.9	58	3	US-09-414-878-103
13	10	5.9	58	3	US-09-240-136-93
14	10	5.9	58	3	US-09-240-136-103
15	9	5.3	58	1	US-08-358-160-116
16	9	5.3	58	3	US-08-676-124-111
17	9	5.3	58	3	US-09-414-878-111
18	9	5.3	58	3	US-09-240-136-111
19	9	5.3	59	5	5466783-6
20	9	5.3	65	1	US-08-358-160-92
21	9	5.3	65	5	5466783-12
22	8	4.7	58	1	US-08-463-155A-61
23	8	4.7	58	1	US-08-463-432B-61
24	8	4.7	58	3	US-08-676-124-96
25	8	4.7	58	3	US-09-414-878-96
26	8	4.7	58	3	US-09-240-136-96
27	7	4.1	41	2	US-08-640-847C-41
28	7	4.1	57	1	US-08-358-160-126

29 7 4.1 57 2 US-08-829-876-152 Sequence 152, Appl
30 7 4.1 58 1 US-08-321-658B-4 Sequence 4, Appl
31 7 4.1 58 1 US-08-321-658B-5 Sequence 5, Appl
32 7 4.1 58 1 US-08-463-155A-1 Sequence 1, Appl
33 7 4.1 58 1 US-08-463-155A-2 Sequence 2, Appl
34 7 4.1 58 1 US-08-463-155A-3 Sequence 3, Appl
35 7 4.1 58 1 US-08-463-155A-4 Sequence 4, Appl
36 7 4.1 58 1 US-08-463-155A-45 Sequence 45, Appl
37 7 4.1 58 1 US-08-463-155A-46 Sequence 46, Appl
38 7 4.1 58 1 US-08-463-155A-47 Sequence 47, Appl
39 7 4.1 58 1 US-08-463-155A-48 Sequence 48, Appl
40 7 4.1 58 1 US-08-463-155A-49 Sequence 49, Appl
41 7 4.1 58 1 US-08-463-155A-50 Sequence 50, Appl
42 7 4.1 58 1 US-08-463-155A-51 Sequence 51, Appl
43 7 4.1 58 1 US-08-463-155A-52 Sequence 52, Appl
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45 7 4.1 58 1 US-08-463-155A-54 Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-08-685-660A-7
; Sequence 7, Application US/08685660A
; Patent No. 5731412
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,660A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hei 7-187134
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kit, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: O-42295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-660A-7

Query Match 100.0%; Score 170; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 7.5e-150;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRGRCASMPRWNTVDTGSCQLFVYGCDCGNSNNYLTKECLKK 60
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DB 28 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKKECLK 87

QY 61 CATVTENATGDLATSRNAADSSVPSAPRQDSEHSDMFNEEYCTANAVTGPCRASFP 120

DB 88 CATVTENATGDLATSRNAADSSVPSAPRQDSEHSDMFNEEYCTANAVTGPCRASFP 147

QY 121 RWYFDVERNSCNFFIYGGCGKNSYRSEACMLRCFRQENPPLPLGSK 170

DB 148 RWYFDVERNSCNFFIYGGCGKNSYRSEACMLRCFRQENPPLPLGSK 197

RESULT 2

US-08-974-196-7

Sequence 7, Application US/08974196

Patent No. 5854396

GENERAL INFORMATION:

APPLICANT: SHIMOMURA, Takeshi

APPLICANT: KAWAGUCHI, Toshiya

APPLICANT: KITAMURA, Naomi

TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME

TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974.196

FILING DATE: 24-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JPA Hei 7-187134

FILING DATE: 24-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: Q-42295

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-974-196-7

Query Match 100.0%; Score 170; DB 2; Length 252;

Best Local Similarity 100.0%; Pred. No. 7.5e-150;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKKECLK 60

DB 28 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKKECLK 87

QY 61 CATVTENATGDLATSRNAADSSVPSAPRQDSEHSDMFNEEYCTANAVTGPCRASFP 120

DB 88 CATVTENATGDLATSRNAADSSVPSAPRQDSEHSDMFNEEYCTANAVTGPCRASFP 147

QY 121 RWYFDVERNSCNFFIYGGCGKNSYRSEACMLRCFRQENPPLPLGSK 170

DB 148 RWYFDVERNSCNFFIYGGCGKNSYRSEACMLRCFRQENPPLPLGSK 197

RESULT 3

US-08-685-660A-3

Sequence 3, Application US/08685660A

Patent No. 5731412

GENERAL INFORMATION:

APPLICANT: SHIMOMURA, Takeshi

APPLICANT: KAWAGUCHI, Toshiya

APPLICANT: KITAMURA, Naomi

TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME

TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,660A

FILING DATE: 24-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JPA Hei 7-187134

FILING DATE: 24-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: Q-42295

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal fragment

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

STRAIN: MKN45

US-08-685-660A-3

Query Match 15.3%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.4e-17;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 ATVTENATGDLATSRNAADSSVPSAP 87

DB 1 ATVTENATGDLATSRNAADSSVPSAP 26

RESULT 4

US-08-974-196-3

Sequence 3, Application US/08974196

Patent No. 5854396

GENERAL INFORMATION:

APPLICANT: SHIMOMURA, Takeshi

APPLICANT: KAWAGUCHI, Toshiya

APPLICANT: KITAMURA, Naomi

TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME

TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

Wed Jan 31 15:14:32 2001

us-09-441-654a-1.oli.ra1

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; STRAIN: MKN45
US-08-974-196-2

Query Match 8.8%; Score 15; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

Qy 21 RASMPRWYNTDGS 35
Db 7 RASMPRWYNTDGS 21

RESULT 7
US-08-685-660A-1
; Sequence 1, Application US/08685660A
; Patent No. 5731412
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,660A
FILING DATE: 24-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA Hei 7-187134
FILING DATE: 24-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: Q-42295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal fragment
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
US-08-685-660A-1

Query Match 5.9%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

Qy 1 ADRERSIHDF 10

Db 1 ADRERSIHDF 10

RESULT 8
US-08-974-196-1
; Sequence 1, Application US/08974196
; Patent No. 5854396
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,196
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,660
FILING DATE: 24-JUL-1996
APPLICATION NUMBER: JPA Hei 7-187134
FILING DATE: 24-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: Q-42295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal fragment
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
US-08-974-196-1

Query Match 5.9%; Score 10; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

Qy 1 ADRERSIHDF 10
Db 1 ADRERSIHDF 10

RESULT 9
US-08-676-124-93
; Sequence 93, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS

NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND=3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-93

Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 113 GPCRASFPWW 122
C 12 GPCRASFPWW 21
|||||

RESULT 10
US-08-676-124-103
Sequence 103, Application US/08676124
Patent No. 6010880
GENERAL INFORMATION:
APPLICANT: MARKLAND, William
ADDRESSEE: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND=3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-103

Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 112 TGPCRASFPR 121
D 11 TGPCRASFPR 20
|||||

RESULT 11
US-09-414-878-93
Sequence 93, Application US/09414878
Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
ADDRESSEE: Yankwich & Associates
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 43,310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-8801
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-414-878-93

Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 GPCRSPRPW 122
| | | | | | | | | |
DB 12 GPCRSPRPW 21

RESULT 12
US-09-414-878-103
; Sequence 103, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,878
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/240,136
; FILING DATE: 29-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 43,310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-8801
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-414-878-103

Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 TGPCRASFPR 121
| | | | | | | | | |
DB 11 TGPCRASFPR 20

RESULT 13
US-09-240-136-93
; Sequence 93, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-93

Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 GPCRASFPWR 122
Db 12 GPCRASFPWR 21

RESULT 14
US-09-240-136-103
Sequence 103, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,695
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-103
Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 112 TGPCRASFPFR 121
Db 11 TGPCRASFPFR 20
RESULT 15
US-08-358-160-116
Sequence 116, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-116

Query Match 5.3%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 FIYGGCRGN 142
| | | | |
Db 35 FIYGGCRGN 43

Search completed: January 31, 2001, 15:06:02
Job time: 103 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:04:16 ; Search time 16.78 seconds
(without alignments)
346.421 Million cell updates/sec

Title: US-09-441-654A-1

Perfect score: 170

Sequence: 1 ADERSIHDFCLVSKVGRG.....ACMLRCFRQENPPLPLGSK 170

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 268485 seqs, 34193795 residues

d size : 0

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	170	W30041	Human placental bi
2	170	100.0	179	W30053	Human placental bi
3	170	100.0	197	W30043	Human placental bi
4	170	100.0	213	W30042	Human placental bi
5	170	100.0	225	W30046	Human placental bi
6	170	100.0	235	W30060	Human placental bi
7	170	100.0	240	W30045	Human placental bi
8	170	100.0	248	W30044	Human placental bi
9	170	100.0	252	W30040	Human placental bi
10	170	100.0	252	W13665	Hepatocyte growth
11	170	100.0	252	W70286	Human tissue facto
12	153	90.0	153	W30051	Human placental bi

13	146	85.9	146	18	W30052	Human placental bi
14	92	54.1	92	18	W30054	Human placental bi
15	84	49.4	169	18	W30062	EST R74593 protein
16	72	42.4	130	18	W30047	EST R35464 protein
17	58	34.1	58	18	W30049	Human placental bi
18	58	34.1	58	18	W30049	Human placental bi
19	51	30.0	51	18	W30048	Human placental bi
20	51	30.0	51	18	W30050	Human placental bi
21	38	22.4	170	18	W30061	Human consensus bi
22	26	15.3	26	18	W13664	Hepatocyte growth
23	15	8.8	29	18	W13663	Hepatocyte growth
24	11	6.5	302	14	R35001	LACI. Rattus rat
25	11	6.5	302	17	R88513	Lipoprotein-associ
26	10	5.9	12	16	R78576	LACI K1 derivative
27	10	5.9	12	16	R78586	LACI K1 derivative
28	10	5.9	15	16	W13662	Hepatocyte growth
29	9	5.3	12	16	R78594	LACI K1 derivative
30	8	4.7	12	16	R78579	LACI K1 derivative
31	8	4.7	58	18	W07766	Non-native Kunitz-
32	8	4.7	58	19	W64138	Human Kunitz-type
33	8	4.7	219	21	Y54090	Enzyme EFSE involv
34	8	4.7	219	21	Y43792	Amino acid sequenc
35	7	4.1	12	16	R78578	LACI K1 derivative
36	7	4.1	56	14	R39677	C-terminal Kunitz-
37	7	4.1	57	11	R08293	Example of Alzheim
38	7	4.1	57	19	W47434	Aprotinin variant
39	7	4.1	57	19	W47435	Aprotinin variant
40	7	4.1	57	19	W47436	Aprotinin variant
41	7	4.1	57	21	Y68103	C-terminal Kunitz-
42	7	4.1	58	14	R39673	Kunitz-type protea
43	7	4.1	58	14	R39799	Kunitz-type protea
44	7	4.1	58	14	R39800	Kunitz-type protea
45	7	4.1	58	16	R78556	Human III-Kudow 2

ALIGNMENTS

RESULT 1
W30041
ID W30041 standard; Protein; 170 AA.

AC W30041;
DT 20-APR-1998 (first entry)
DE Human placental bikunin.
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
OS Homo sapiens.
XX
XX
XX WO9733996-A2.
XX
XX 18-SEP-1997.
XX
XX 10-MAR-1997; 97WO-US03894.
XX
XX 04-OCT-1996; 96US-0725251.
XX 11-MAR-1996; 96US-0013106.
XX 14-JUN-1996; 96US-0019793.
XX (FARB) BAYER CORP.
XX
XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP.
XX WPI; 1997-470876/43.
XX

PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss

XX Claim 1; Page 65; 110pp; English.

XX The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.

XX Sequence 170 AA;

Query Match 100.0%; Score 170; DB 18; Length 170;

. Best Local Similarity 100.0%; Pred. No. 2.4e-156;

. Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSOLFVYGGDGNNSNYLTKEECLK 60

DB 1 adersihdfclvskvvgrcrasmprrwvntdgsqclfvvgcdgnsnnyltkeecik 60

QY 61 CATVTENATGLATSRNAADSSVPSAPRRQDSEHSDMFNIEYCTANAVTGPCRASFP 120

DB 61 catvtenatglatrnaadssvpsaprrqdsedhssdmfnyeyctananavtgcrafp 120

QY 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170

DB 121 rwyfdvernsnfnfyggcrgnknsyrseacmlrcfrqenpplplgsk 170

RESULT 2

W30053

W30053 standard; Protein; 179 AA.

W30053;

DT 20-APR-1998 (first entry)

Human placental bikunin.

Human; placental bikunin; inhibition; trypsin; kallikrein;
 plasmin; factor XIIa; treatment; prevention; oedema;
 inflammation; infection; granulomatosis; multiple sclerosis;
 ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 blood coagulation disease; polytrauma; stroke; haemorrhage;
 gastric cancer; cervical cancer; metastasis; blood loss.

OS Homo sapiens.

PN W09733996-A2.

PD 18-SEP-1997.

PF 10-MAR-1997; 97WO-0503894.

PR 04-OCT-1996; 96US-0725251.

PR 11-MAR-1996; 96US-0013106.

PR 14-JUN-1996; 96US-0019793.

PA (FARB) BAYER CORP.

PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

XX WPI; 1997-470876/43.

XX New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss

XX Claim 1; Page 67; 110pp; English.

XX The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.

XX Sequence 179 AA;

Query Match 100.0%; Score 170; DB 18; Length 179;

. Best Local Similarity 100.0%; Pred. No. 2.5e-156;

. Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSOLFVYGGDGNNSNYLTKEECLK 60

DB 1 adersihdfclvskvvgrcrasmprrwvntdgsqclfvvgcdgnsnnyltkeecik 60

QY 61 CATVTENATGLATSRNAADSSVPSAPRRQDSEHSDMFNIEYCTANAVTGPCRASFP 120

DB 61 catvtenatglatrnaadssvpsaprrqdsedhssdmfnyeyctananavtgcrafp 120

QY 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170

DB 121 rwyfdvernsnfnfyggcrgnknsyrseacmlrcfrqenpplplgsk 170

RESULT 3

W30043

ID W30043 standard; Protein; 197 AA.

XX W30043;

DT 20-APR-1998 (first entry)

XX Human placental bikunin.

Human; placental bikunin; inhibition; trypsin; kallikrein;
 plasmin; factor XIIa; treatment; prevention; oedema;
 inflammation; infection; granulomatosis; multiple sclerosis;
 ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 blood coagulation disease; polytrauma; stroke; haemorrhage;
 gastric cancer; cervical cancer; metastasis; blood loss.

OS Homo sapiens.

W09733996-A2.

18-SEP-1997.

10-MAR-1997; 97WO-US03894.

04-OCT-1996; 96US-0725251.

11-MAR-1996; 96US-0013106.

14-JUN-1996; 96US-0019793.

(FARB) BAYER CORP.

Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

WPI; 1997-470876/43.

New human placental bikunin - used to inhibit kallikrein, trypsin etc. in treatment of oedema, multiple sclerosis, fibrosis, or perioperative blood loss

Claim 1; Page 65; 110pp; English.

The present sequence is a human placental bikunin, which inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa. Bikunin can be used to treat or prevent brain and spinal cord oedema, inflammation, infection or granulomatosis, multiple sclerosis, ischaemia, perioperative blood loss, sepsis, shock, fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral or subarachnoid haemorrhage and gastric or cervical cancer and prevent metastasis. It is particularly useful for reducing blood loss during surgery, and can also be used to treat other cancer, arthritis, anaemia, non-insulin dependent diabetes, influenza and similar viral infections, acute pancreatitis and gout, and prevent pre-term labour. It has similar properties to aprotinin, but is less highly charged so should be less immunogenic and less likely to damage the kidneys. Manipulation of the bikunin sequence may allow the inhibitory profile to be altered. It also reduces or eliminates the need for whole donor blood or blood products during surgery, thereby reducing the risk of infection and other adverse side effects, as well as reducing the cost of surgery.

Sequence 197 AA;

Query Match 100.0%; Score 170; DB 18; Length 197;
Best Local Similarity 100.0%; Pred. No. 2,7e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ADERSIHDCLVSKVVGRCRASPMPRWYNTDGSOLFVYGGCDGNSNNYLTKEECLKK 60

19 adersihdclvskvvgrcrasmprrwvntdgsqqlfvyggcdgnsnnyltkeecclk 78

61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEYECTANAVTGPCRASFP 120

79 catvtenatgdlatsrnaadssvpsaprrqdsdhsdmdfneyectanavtgpccrasfp 138

121 RWFYDVERNSCNFFYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170

139 rwyfdvernsnfnfyggcrgnknysrseacmlrcfrqenpplplgsk 188

RESULT 4

W30042

ID W30042 standard; Protein; 213 AA.

AC W30042;

20-APR-1998 (first entry)

Human placental bikunin.

Human; placental bikunin; inhibition; trypsin; kallikrein;

KW

KW plasmin; factor XIIa; treatment; prevention; oedema;

KW inflammation; infection; granulomatosis; multiple sclerosis;

KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;

KW blood coagulation disease; polytrauma; stroke; haemorrhage;

KW gastric cancer; cervical cancer; metastasis; blood loss.

XX Homo sapiens.

XX OS

XX W09733996-A2.

XX PN

XX 18-SEP-1997.

XX PD

XX 10-MAR-1997; 97WO-US03894.

XX PF

XX 04-OCT-1996; 96US-0725251.

XX PR

XX 11-MAR-1996; 96US-0013106.

XX PR

XX 14-JUN-1996; 96US-0019793.

XX PA

XX (FARB) BAYER CORP.

XX PI

XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

XX WPI; 1997-470876/43.

XX DR

XX New human placental bikunin - used to inhibit kallikrein, trypsin

XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or

XX perioperative blood loss

XX PS

XX Claim 1; Page 65; 110pp; English.

XX XX

XX The present sequence is a human placental bikunin, which

XX inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.

XX Bikunin can be used to treat or prevent brain and spinal cord

XX oedema, inflammation, infection or granulomatosis, multiple

XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,

XX fibrosis, blood coagulation diseases, polytrauma, stroke,

XX cerebral or subarachnoid haemorrhage and gastric or cervical

XX cancer and prevent metastasis. It is particularly useful for

XX reducing blood loss during surgery, and can also be used to treat

XX other cancer, arthritis, anaemia, non-insulin dependent diabetes,

XX influenza and similar viral infections, acute pancreatitis and

XX gout, and prevent pre-term labour. It has similar properties to

XX aprotinin, but is less highly charged so should be less

XX immunogenic and less likely to damage the kidneys. Manipulation

XX of the bikunin sequence may allow the inhibitory profile to be

XX altered. It also reduces or eliminates the need for whole donor

XX blood or blood products during surgery, thereby reducing the risk

XX of infection and other adverse side effects, as well as reducing

XX the cost of surgery.

XX CC

XX Sequence 213 AA;

Query Match

Best Local Similarity 100.0%; Score 170; DB 18; Length 213;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADERSIHDCLVSKVVGRCRASPMPRWYNTDGSOLFVYGGCDGNSNNYLTKEECLKK 60

Db 1 adersihdclvskvvgrcrasmprrwvntdgsqqlfvyggcdgnsnnyltkeecclk 60

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEYECTANAVTGPCRASFP 120

Db 61 catvtenatgdlatsrnaadssvpsaprrqdsdhsdmdfneyectanavtgpccrasfp 120

Qy 121 RWFYDVERNSCNFFYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170

Db 121 rwyfdvernsnfnfyggcrgnknysrseacmlrcfrqenpplplgsk 170

RESULT 5

W30046

ID W30046 standard; Protein; 225 AA.

```
XX AC W30046;
XX DT 20-APR-1998 (first entry)
XX DE Human placental bikunin.
XX KW Human: placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX OS Homo sapiens.
XX KW Human: consensus bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 198 /note= "encoded by TGA"
FT Misc-difference 201 /note= "encoded by TGA"
FT Misc-difference 226 /note= "encoded by GAN"
FT Misc-difference 233 /note= "encoded by TGA"
FT XX WO9733996-A2.
XX PN Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX DT WPI; 1997-470876/43.
XX PT New human placental bikunin - used to inhibit kallikrein, trypsin
XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX perioperative blood loss
XX PS Claim 1; Page 66; 110pp; English.
XX CC The present sequence is a human placental bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
XX Bikunin can be used to treat or prevent brain and spinal cord
XX oedema, inflammation, infection or granulomatosis, multiple
XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX fibrosis, blood coagulation diseases, polytrauma, stroke,
XX cerebral or subarachnoid haemorrhage and gastric or cervical
XX cancer and prevent metastasis. It is particularly useful for
XX reducing blood loss during surgery, and can also be used to treat
XX other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX influenza and similar viral infections, acute pancreatitis and
XX gout, and prevent pre-term labour. It has similar properties to
XX aprotinin, but is less highly charged so should be less
XX immunogenic and less likely to damage the kidneys. Manipulation
XX of the bikunin sequence may allow the inhibitory profile to be
XX altered. It also reduces or eliminates the need for whole donor
XX blood or blood products during surgery, thereby reducing the risk
XX of infection and other adverse side effects, as well as reducing
XX the cost of surgery.
XX SQ Sequence 225 AA;
Query Match 100.0%; Score 170; DB 18; Length 225;
Best Local Similarity 100.0%; Pred. No. 3e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSHDFCLVSKVGRASPRWYNTDSCGLFYVGGDGSNNYLTKECLKK 60
DB 1 aderslhdclvskvgrcrasprwyyntdsgclfyv99cdgnsnyltkeecllk 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRODSEHSDSMFNYEYCYANAVTGPCRASFP 120
DB 61 catvtenatgdlatsrnaadssvpsaprrqdsedhsdmsmfneyeyctanavtgcrafp 120
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QY 121 RWFYDVERNSCNFIYGGCRGNKNSYSEACMLRCFRQOENPPLPLGSK 170
DB 121 rwyfdvernschnfiyggcrgnknysrseeacmlrcfrqenpplp.lgsk 170
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RESULT 6
W30060
ID W30060 standard: Protein; 235 AA.
XX AC W30060;
XX DT 20-APR-1998 (first entry)
XX DE Human consensus bikunin.
XX KW Human: consensus bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX OS Homo sapiens.
```

```
Key Location/Qualifiers
FT Misc-difference 198 /note= "encoded by TGA"
FT Misc-difference 201 /note= "encoded by TGA"
FT Misc-difference 226 /note= "encoded by GAN"
FT Misc-difference 233 /note= "encoded by TGA"
FT XX WO9733996-A2.
XX PN Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX DT WPI; 1997-470876/43.
XX PT New human placental bikunin - used to inhibit kallikrein, trypsin
XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX perioperative blood loss
XX PS Disclosure; Fig 3; 110pp; English.
XX CC The present sequence is a consensus human bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
XX Bikunin can be used to treat or prevent brain and spinal cord
XX oedema, inflammation, infection or granulomatosis, multiple
XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX fibrosis, blood coagulation diseases, polytrauma, stroke,
XX cerebral or subarachnoid haemorrhage and gastric or cervical
XX cancer and prevent metastasis. It is particularly useful for
XX reducing blood loss during surgery, and can also be used to treat
XX other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX influenza and similar viral infections, acute pancreatitis and
XX gout, and prevent pre-term labour. It has similar properties to
XX aprotinin, but is less highly charged so should be less
XX immunogenic and less likely to damage the kidneys. Manipulation
XX of the bikunin sequence may allow the inhibitory profile to be
XX altered. It also reduces or eliminates the need for whole donor
XX blood or blood products during surgery, thereby reducing the risk
XX of infection and other adverse side effects, as well as reducing
XX the cost of surgery.
```

```
XX CC The present sequence is a consensus human bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
XX Bikunin can be used to treat or prevent brain and spinal cord
XX oedema, inflammation, infection or granulomatosis, multiple
XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX fibrosis, blood coagulation diseases, polytrauma, stroke,
XX cerebral or subarachnoid haemorrhage and gastric or cervical
XX cancer and prevent metastasis. It is particularly useful for
XX reducing blood loss during surgery, and can also be used to treat
XX other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX influenza and similar viral infections, acute pancreatitis and
XX gout, and prevent pre-term labour. It has similar properties to
XX aprotinin, but is less highly charged so should be less
XX immunogenic and less likely to damage the kidneys. Manipulation
XX of the bikunin sequence may allow the inhibitory profile to be
XX altered. It also reduces or eliminates the need for whole donor
```

CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 170; DB 18; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.1e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRASMPRWYNTDSCOLFVYGGDGNNSNYLTKEECLKK 60
Db 19 adersihdfclvskvgrasmprrwvntdgsclfvvgcdgnsnyltkeecclkk 78
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASFP 120
Db 79 catvtenatgdlatsrnaadssvpsaprrqdsdhsdmfneeyctanavtgpccrasfp 138
121 RWYFDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
139 rwyfdvernsnfnfiyggcrngknsyrseacmlrcfrqenpplplgsk 188

RESULT 7
W30045
ID W30045 standard; Protein; 240 AA.

AC W30045;
XX 20-APR-1998 (first entry)

DE Human placental bikunin.

Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.

OS Homo sapiens.

PN WO9733996-A2.

PD 18-SEP-1997.

PF 10-MAR-1997; 97WO-US03894.

PR 04-OCT-1996; 96US-0725251.

PR 11-MAR-1996; 96US-0013106.

PR 14-JUN-1996; 96US-0019793.

PA (FARB) BAYER CORP.

XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

XX WPI; 1997-470876/43.

XX N-PSDB; T90734.

XX New human placental bikunin - used to inhibit kallikrein, trypsin
XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX perioperative blood loss

XX Claim 1; Page 66; 110pp; English.

XX The present sequence is human placental bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
XX Bikunin can be used to treat or prevent brain and spinal cord
XX oedema, inflammation, infection or granulomatosis, multiple
XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX fibrosis, blood coagulation diseases, polytrauma, stroke,
XX cerebral or subarachnoid haemorrhage and gastric or cervical

CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
XX the cost of surgery.

XX Sequence 240 AA;

Query Match 100.0%; Score 170; DB 18; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRASMPRWYNTDSCOLFVYGGDGNNSNYLTKEECLKK 60
Db 28 adersihdfclvskvgrasmprrwvntdgsclfvvgcdgnsnyltkeecclkk 87

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASFP 120
Db 88 catvtenatgdlatsrnaadssvpsaprrqdsdhsdmfneeyctanavtgpccrasfp 147

QY 121 RWYFDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
Db 148 rwyfdvernsnfnfiyggcrngknsyrseacmlrcfrqenpplplgsk 197

RESULT 8

W30044

ID W30044 standard; Protein; 248 AA.

XX W30044;

XX 20-APR-1998 (first entry)

XX Human consensus bikunin.

Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.

OS Homo sapiens.

PN WO9733996-A2.

PD 18-SEP-1997.

PF 10-MAR-1997; 97WO-US03894.

PR 04-OCT-1996; 96US-0725251.

PR 11-MAR-1996; 96US-0013106.

PR 14-JUN-1996; 96US-0019793.

PA (FARB) BAYER CORP.

XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

XX WPI; 1997-470876/43.

XX N-PSDB; T90733.

XX New human placental bikunin - used to inhibit kallikrein, trypsin
XX etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX perioperative blood loss

Claim 1; page 66; 110pp; English.

The present sequence is a consensus human bikunin, which inhibits, e.g. trypsin, kallikrein, plasmin and factor Xlla. Bikunin can be used to treat or prevent brain and spinal cord oedema, inflammation, infection or granulomatosis, multiple sclerosis, ischaemia, peroperative blood loss, sepsis, shock, fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral or subarachnoid haemorrhage and gastric or cervical cancer and prevent metastasis. It is particularly useful for reducing blood loss during surgery, and can also be used to treat other cancer, arthritis, anaemia, non-insulin dependent diabetes, influenza and similar viral infections, acute pancreatitis and gout, and prevent pre-term labour. It has similar properties to aprotinin, but is less highly charged so should be less immunogenic and less likely to damage the kidneys. Manipulation of the bikunin sequence may allow the inhibitory profile to be altered. It also reduces or eliminates the need for whole donor blood or blood products during surgery, thereby reducing the risk of infection and other adverse side effects, as well as reducing the cost of surgery.

Sequence 248 AA:

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Very Match      100.0%; Score 170; DB 18; Length 248;
1st Local Similarity 100.0%; Pred. No. 3.2e-156;
atches 170; Conservative 0; Mismatches 0; Indels 0

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[illegible]

61 CATVTENATGDLATSNAAADSSVPSAPRRQDSEHSSDMFNVEEYCTANAVTGPCRASF 120
 |||||
 84 catvtENatgdlatsnAAADssvpsAPRRQdseHSSdmfnveeYctANAVtGpCRasf 143

121 RWYFDVERNSCNFIYGGCRGNKNSYRSEEAACMLRCFRQENPPLPLGSK 170
 |||||
 144 rwyfðvernschnfiyagcrgnknsvrseeaclrcfrqenpplplgsk 193

LT 9
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W30040 standard: Protein: 252 AA.

W30040;

20-APR-1998 (first entry)

Human placental bikunin.

Human; placental bikunin; inhibition; trypsin; kallikrein; plasmin; factor xIIa; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.

Homo sapiens.

WO9733996-A2.

18-SEP-1997.

10-MAR-1997; 97WO-US03894.

04-OCT-1996; 96US-0725251.

14-JUN-1996; 96US-0019793.

(FARB) BAYER CORP.

Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;

WPI; 1997-470876/43.

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etc. in treatment of oedema, multiple sclerosis, fibrosis, or peroperative blood loss

Claim 1; Page 65; 110pp; English.

The present sequence is a human placental bikunin, which inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa. Bikunin can be used to treat or prevent brain and spinal cord oedema, inflammation, infection or granulomatosis, multiple sclerosis, ischaemia, perioperative blood loss, sepsis, shock, fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral or subarachnoid haemorrhage and gastric or cervical cancer and prevent metastasis. It is particularly useful for reducing blood loss during surgery, and can also be used to treat other cancer, arthritis, anaemia, non-insulin dependent diabetes, influenza and similar viral infections, acute pancreatitis and gout, and prevent pre-term labour. It has similar properties to aprotinin, but is less highly charged so should be less immunogenic and less likely to damage the kidneys. Manipulation of the bikunin sequence may allow the inhibitory profile to be altered. It also reduces or eliminates the need for whole donor blood or blood products during surgery, thereby reducing the risk of infection and other adverse side effects, as well as reducing the cost of surgery.

Sequence 252 AA;

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every Match      100.0%; Score 170; DB 18; Length 252;
1st Local Similarity 100.0%; Pred. No. 3.3e-156;
Matches 170: Conservative 0; Mismatches 0; Indels 0

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1 ADERSIHDFCLSVKVGRCRASMPRWYNVTGSCQLFVYGGCDGSNNYLTKKECLKK 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
28 adersihdfclsvkvgrcrasmpwvntqscqlfvvagcdgsnnyltkkeclk 87
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61 CATYFENATGDIATSRNAADSSVPSAPRRDSEDHSSDMFNVEEYCTANAVTGPCRASEP 120

88 catvttenatqdlatsrnaadssvpsaprrqdsedhssdmfnyeeeyctanavtgp

LT 10

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Hepatocyte growth factor activator inhibitor; HAI-II; HGF; human;

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THE UNIVERSITY OF CHICAGO

Peptide
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XX OS Homo sapiens.
XX PN WO9733996-A2.
XX PD 18-SEP-1997.
XX PF 10-MAR-1997; 97WO-US03894.
XX PR 04-OCT-1996; 96US-0725251.
XX PR 11-MAR-1996; 96US-0013106.
XX PR 14-JUN-1996; 96US-0019793.
XX PA (FARB ) BAYER CORP.
XX PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX DR WPI; 1997-470876/43.
XX PT New human placental bikunin - used to inhibit kallikrein, trypsin
XX PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX PT perioperative blood loss
XX PS Claim 1; Page 67; 110pp; English.
XX CC The present sequence is a human placental bikunin, which
XX CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
XX CC Bikunin can be used to treat or prevent brain and spinal cord
XX CC oedema, inflammation, infection or granulomatosis, multiple
XX CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX CC fibrosis, blood coagulation diseases, polytrauma, stroke,
XX CC cerebral or subarachnoid haemorrhage and gastric or cervical
XX CC cancer and prevent metastasis. It is particularly useful for
XX CC reducing blood loss during surgery, and can also be used to treat
XX CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX CC influenza and similar viral infections, acute pancreatitis and
XX CC gout, and prevent pre-term labour. It has similar properties to
XX CC aprotinin, but is less highly charged so should be less
XX CC immunogenic and less likely to damage the kidneys. Manipulation
XX CC of the bikunin sequence may allow the inhibitory profile to be
XX CC altered. It also reduces or eliminates the need for whole donor
XX CC blood or blood products during surgery, thereby reducing the risk
XX CC of infection and other adverse side effects, as well as reducing
XX CC the cost of surgery.
XX CC Sequence 153 AA;
XX
XX Query Match 90.0%; Score 153; DB 18; Length 153;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-140;
XX Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 7 IHDFCLVSKVVGCRASMPRWYVNTDGSQCLFYVGGCDGNSNNYLTKEECLKKCATVTE 66
Db 1 ihdfclvskvvgcrasmprrwvntdgsqclfyvggcdgnsnnyltkeec.lkcatvte 60
OY 67 NATGDLATSRNAADSSVPSAPRRDSDHSDMFNYEYCTANAVTGPCRASFPFRWYFDV 126
Db 61 natgdlatrnaadssvpsaprrdgsdhsdmfnyeyctanavtgpccrasfprwfyfdv 120
OY 127 ERNSCNFFIYGGCRGNKNSYRSEACMLRCFRQ 159
Db 121 ernscnnffiyggcrgnknsyrseacmlrcfrq 153
RESULT 13
W30052
ID W30052 standard; Protein; 146 AA.
XX AC W30052;
XX XX
XX DT 20-APR-1998 (first entry)
XX XX
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```
DE XX Human placental bikunin.
KW KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
OS Homo sapiens.
XX XX WO9733996-A2.
XX PD 18-SEP-1997.
XX PF 10-MAR-1997; 97WO-US03894.
XX PR 04-OCT-1996; 96US-0725251.
XX PR 11-MAR-1996; 96US-0013106.
XX PR 14-JUN-1996; 96US-0019793.
XX PA (FARB ) BAYER CORP.
XX PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX DR WPI; 1997-470876/43.
XX PT New human placental bikunin - used to inhibit kallikrein, trypsin
XX PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX PT perioperative blood loss
XX PS Claim 1; Page 67; 110pp; English.
XX CC The present sequence is a human placental bikunin, which
XX CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
XX CC Bikunin can be used to treat or prevent brain and spinal cord
XX CC oedema, inflammation, infection or granulomatosis, multiple
XX CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX CC fibrosis, blood coagulation diseases, polytrauma, stroke,
XX CC cerebral or subarachnoid haemorrhage and gastric or cervical
XX CC cancer and prevent metastasis. It is particularly useful for
XX CC reducing blood loss during surgery, and can also be used to treat
XX CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX CC influenza and similar viral infections, acute pancreatitis and
XX CC gout, and prevent pre-term labour. It has similar properties to
XX CC aprotinin, but is less highly charged so should be less
XX CC immunogenic and less likely to damage the kidneys. Manipulation
XX CC of the bikunin sequence may allow the inhibitory profile to be
XX CC altered. It also reduces or eliminates the need for whole donor
XX CC blood or blood products during surgery, thereby reducing the risk
XX CC of infection and other adverse side effects, as well as reducing
XX CC the cost of surgery.
XX CC Sequence 146 AA;
XX
XX Query Match 85.9%; Score 146; DB 18; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-133;
XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 11 CLVSKVVGCRASMPRWYVNTDGSQCLFYVGGCDGNSNNYLTKEECLKKCATVTEATG 70
Db 1 clvskvvgcrasmprrwvntdgsqclfyvggcdgnsnnyltkeec.lkcatvtenatg 60
OY 71 DLATSRNAADSSVPSAPRRDSDHSDMFNYEYCTANAVTGPCRASFPFRWYFDV 130
Db 61 dlatsrnaadssvpsaprrdgsdhsdmfnyeyctanavtgpccrasfprwfyfdv 120
OY 131 CNNFIYGGCRGNKNSYRSEACMLRC 156
Db 121 cnnfiyggcrgnknsyrseacmlrc 146
```

Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92

RESULT 15
#30054 W30054 standard; Protein; 92 AA.
W30054;
20-APR-1998 (first entry)
Human placental bikunin.

XX Human; placental bikunin; inhibition; trypsin; kallikrein;
XX plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
XX Homo sapiens.
OS WO9733996-A2.
18-SEP-1997.
XX 10-MAR-1997; 97WO-US03894.
XX 04-OCT-1996; 96US-0725251.
XX 11-MAR-1996; 96US-0013106.
XX 14-JUN-1996; 96US-0019793.
XX (FARB) BAYER CORP.
XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
PI WPI; 1997-470876/43.
XX New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
XX Claim 1: Page 67; 110pp; English.
XX The present sequence is a human placental bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
XX Bikunin can be used to treat or prevent brain and spinal cord
XX oedema, inflammation, infection or granulomatosis, multiple
XX sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
XX fibrosis, blood coagulation diseases, polytrauma, stroke,
XX cerebral or subarachnoid haemorrhage and gastric or cervical
XX cancer and prevent metastasis. It is particularly useful for
XX reducing blood loss during surgery, and can also be used to treat
XX other cancer, arthritis, anaemia, non-insulin dependent diabetes,
XX influenza and similar viral infections, acute pancreatitis and
XX gout, and prevent pre-term labour. It has similar properties to
XX aprotinin, but is less highly charged so should be less
XX immunogenic and less likely to damage the kidneys. Manipulation
XX of the bikunin sequence may allow the inhibitory profile to be
XX altered. It also reduces or eliminates the need for whole donor
XX blood or blood products during surgery, thereby reducing the risk
XX of infection and other adverse side effects, as well as reducing
XX the cost of surgery.
XX
XX Sequence 92 AA;
XX
XX Query Match 54.1%; Score 92; DB 18; Length 92;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-81;
XX Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRESIHDFCLVSKVVGRCASMPRWYNVTGSCQLFYVGGDGNNNYLTKECLKK 60
Db 1 adresihdfclvskvvgrcasmprrwvntdgsqclfyvvgdgnnnyltkeclkk 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92

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Query Match          54.1%; Score 92; DB 18; Length 92;
Best Local Similarity 100.0%; Pred. No. 1 9e-81;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSIHDFCLVSKVVGRCASPRWYNTDSCOLFVYGGCDGNSNNYLTKEECLEKK 60
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 adersihdfclvskvvgrcasprwvnyntdsgscqlfvjyggcdgnsnnyltkeeclekk 60
QY 61 CATVTENATGDLATSRNAADSVPSAPRRQDS 92

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